

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 14:02:07 ; Search time 43 Seconds
(without alignments)
694.410 Million cell updates/sec

Title: US-10-759-803-2
Perfect score: 2029
Sequence: 1 MGLNGRRSMKSPPLVLAAL.....DKQRTINLLDQEKRNHTL 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/ECTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2020	99.6	401	US-09-489-847-202	Sequence 202, App
2	2020	99.6	422	US-09-489-847-357	Sequence 357, App
3	631	31.1	148	US-09-673-395A-389	Sequence 389, App
4	168	8.3	3878	US-09-914-259-11	Sequence 11, Appl
5	166.5	8.2	1940	US-09-538-092-901	Sequence 901, App
6	166.5	8.2	1963	US-09-949-016-8888	Sequence 8888, App
7	165.5	8.2	1581	US-09-866-108A-15754	Sequence 15754, A
8	165	8.1	1898	US-08-056-200-94	Sequence 94, Appl
9	165	8.1	1898	US-08-800-644-94	Sequence 94, Appl
10	165	8.1	1898	US-09-538-092-1280	Sequence 1280, Ap
11	161	7.9	1960	US-09-538-092-1077	Sequence 1077, Ap
12	161	7.9	1960	US-09-949-016-10872	Sequence 10872, A
13	160.5	7.9	915	US-09-538-092-863	Sequence 863, App
14	160.5	7.9	916	US-09-949-016-6611	Sequence 6611, App
15	160.5	7.9	916	US-09-949-016-11417	Sequence 11417, A
16	160	7.9	1208	US-09-134-000C-5756	Sequence 5756, Ap
17	159.5	7.9	1695	US-09-866-108A-15753	Sequence 15753, A
18	158.5	7.8	1937	US-09-538-092-918	Sequence 918, App
19	158.5	7.8	2107	US-09-949-016-7646	Sequence 7646, Ap
20	158.5	7.8	2107	US-09-949-016-7647	Sequence 7647, Ap
21	157.5	7.8	2101	US-08-466-390-4	Sequence 4, Appl
22	157.5	7.8	2101	US-08-470-950-4	Sequence 4, Appl
23	157.5	7.8	2101	US-08-467-781-4	Sequence 4, Appl
24	157.5	7.8	2101	US-08-195-487-4	Sequence 4, Appl
25	157.5	7.8	2101	US-08-483-924-4	Sequence 4, Appl
26	157.5	7.8	2101	US-09-452-294-1	Sequence 1, Appl
27	157.5	7.8	2101	PCT-US93-06160-4	Sequence 4, Appl

28	157	7.7	1939	4	US-09-538-092-915	Sequence 915, App
29	157	7.7	1939	4	US-09-949-016-11104	Sequence 11104, A
30	156.5	7.7	1938	4	US-09-949-016-6417	Sequence 6417, Ap
31	156.5	7.7	1959	4	US-09-949-016-8134	Sequence 8134, Ap
32	155	7.6	1979	4	US-09-949-016-6468	Sequence 6468, Ap
33	155	7.6	2047	4	US-09-949-016-7404	Sequence 7404, Ap
34	154.5	7.6	1942	4	US-09-949-016-8135	Sequence 8135, Ap
35	154	7.6	1886	3	US-08-938-105-3	Sequence 3, Appl
36	153.5	7.6	1780	4	US-09-949-016-6899	Sequence 6899, Ap
37	153.5	7.6	1786	4	US-09-949-016-7880	Sequence 7880, Ap
38	153.5	7.6	1939	4	US-09-949-016-6925	Sequence 6925, Ap
39	152	7.5	882	4	US-09-538-092-1036	Sequence 1036, Ap
40	151.5	7.5	793	4	US-09-538-092-1271	Sequence 1271, Ap
41	151.5	7.5	1162	2	US-08-728-323A-2	Sequence 2, Appl
42	151.5	7.5	1162	3	US-09-298-568-2	Sequence 2, Appl
43	151.5	7.5	1162	4	US-09-410-399-2	Sequence 2, Appl
44	151.5	7.5	1162	4	US-09-894-273-2	Sequence 2, Appl
45	151.5	7.5	2186	4	US-09-949-016-10828	Sequence 10828, A

ALIGNMENTS

RESULT 1

US-09-489-847-202
; Sequence 202, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031PI
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 202
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (307)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-489-847-202

Query Match		99.6%	Score 2020;	DB 4;	Length 401;
Best Local Similarity		99.5%	Pred. No. 2e-163;		
Matches 398;		Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	MGLNGRRSMKSPPLVLAALVACIIVLGFTNYWIASRSVDLQTRIMELEGRVRRRAAERG	60		
DB	2	MGLNGRRSMKSPPLVLAALVACIIVLGFTNYWIASRSVDLQTRIMELEGRVRRRAAERG	61		
QY	61	AVELKXNEFQGELEKQREQLDKIOSSHNFQLESVNNKLYQDEKAVLVNNTTGERLIRVLQ	120		
DB	62	AVELKXNEFQGELEKQREQLDKIOSSHNFQLESVNNKLYQDEKAVLVNNTTGERLIRVLQ	121		
QY	121	DOLKTLQNRGLQODVLQFQKQNTNLERKFSYDLSQCNOMKEVKEOCEERIEBVTKKG	180		
DB	122	DOLKTLQNRGLQODVLQFQKQNTNLERKFSYDLSQCNOMKEVKEOCEERIEBVTKKG	181		

Db 1462 LAAALDKKORNF 1474

RESULT 7

US-09-866-108A-15754

; Sequence 15754, Application US/09866108A

; Patent No. 6686188

GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharon G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aemica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 15754

; LENGTH: 1581

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-866-108A-15754

Query Match 8.2%; Score 165.5; DB 4; Length 1581;

Best Local Similarity 22.9%; Pred. No. 5.1e-05;

Matches 96; Conservative 67; Mismatches 151; Indels 105; Gaps 16;

Qy 42 QTRIMELEGRVRRRAAAGAVELKKNFQGELEKQREQLDKI-----QSS 86

Db 1126 QTHSKEMESRDEVEEARQSCQKQKQMEVLEEEVDKQVLRKRELEGLKATLSQV 1185

Qy 87 HNFQLESVNKLQD---EKAVL-----VNNITGRLIRVLQDQI-----123

Db 1186 NRRDFESEKRLKDKLRTKALLADQLMLDLKNSAPSKRETAQKQLESEFTCAAAV 1245

Qy 124 ---KTLQRYNGRLQDVLQFQKQNTNLERKFSYDLSQCNOMKEVKEQCEERIEVTKKG 180

Db 1246 KARKAMEVEIDHLQIDDIKAKTALBEQSLRQREKNEIQNLEEDQEDNNELMKKH 1304

Qy 181 NEAV--ASRDLSENDRQOQLALS-----EPQRLQAAGLPHTPEVQKGNVLGNS---K 231

Db 1305 KAAVAQASRDIAQINDLQAQLEANKQELQKQAL-----QSQVEFLEQSMVDK 1356

Qy 232 SQTPAPSEVLDLSKQVE--KEETNEIQVWNEEPQDRLLPQEPGREGVQVVEDPVGGRGFG 290

Db 1357 SLVSRQEAKEI-----RELETRLEFRTQVRLSLASRLKE--NMKEKLETERD-----1402

Qy 291 GAGELGQTPQVQAALSVSQENPEMGPEDQLVTPDQGEFEQEAAGBGRNQOKLRGEDDY 350

Db 1403 -----QRTAAENREKEQNKRLQRLDRTKTEEMGELARKEAASRKKHLELM 1448

Qy 351 NWDENEARESET-----DKQAALAG---NDRNIDVFNVEDQKRTDITNILLDOR 393

Db 1449 DLESLEAANQSLQADKLAKFKRIGDGLQAIEDMESDENEDLINSEGDSDVDSELEDR 1506

RESULT 8

US-08-056-200-94

; Sequence 94, Application US/08056200

; Patent No. 5616500

GENERAL INFORMATION:

; APPLICANT: Steinert, Peter M.

; APPLICANT: Lee, Seung-Chul

; APPLICANT: Kim, In-Gyu

; APPLICANT: Chung, Soo-Il

; APPLICANT: Park, Sang-Chul

; TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and

; TITLE OF INVENTION: Methods of Using Same

; NUMBER OF SEQUENCES: 117

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive, Sixteenth Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/056,200

FILING DATE: 30-APR-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Fedrick, Michael F.

REGISTRATION NUMBER: 36,799

REFERENCE/DOCKET NUMBER: NIH054.001A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (714) 760-0404

TELEFAX: (714) 760-9502

INFORMATION FOR SEQ ID NO: 94:

SEQUENCE CHARACTERISTICS:

LENGTH: 1898 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-056-200-94

Query Match 8.1%; Score 165; DB 1; Length 1898;

Best Local Similarity 23.2%; Pred. No. 7.3e-05;

Matches 89; Conservative 71; Mismatches 133; Indels 90; Gaps 18;

Qy 49 EGRVRAAAAGAVELKKNFQGELEKQREQLDKIQSSHNFQLESVNKLQDEKAVLYNN 108

Db 593 EQLKREOFERRDQLLKREERROQLKREOFERLE--ORLKREVERLEOEER-----634

Qy 109 ITTGERLIRVLQDQ-----LQNTYGRLOQDVLQFQKQNTNLERKFSYD--LSQC 158

Db 635 ---RDERLKREPEERRRHLLKSEQERRHQLARE--QERRRQRLKREERLEQR 690

Qy 159 INQMKVEQCEERIEEYVTKKGNEAVASR-----DLSENDRQOQLALSPEPRLQA 212

Db 691 LKREHEERREQEELAEQEQAARERIKSRIPKQWQLESEADARQSKVLLAPQ-----A 745

Qy 213 GLPHTVEVQKGNVLGNSKSTPAPSEVLDLSKQVEKEETNEIQVWNEEPQDRLLPQ- 271

Db 746 G--RAEAPQEQ-----EBKRRR-----ESELQWQEERAHRRQQQEEQRDFTWOW 789

QY 272 -----EPGRQVVDPRVGGFGAGELGQTPQVQAALSVSQENPEWEGPERDQVIP 325
DB 790 QAEKESRGRQRLSARPLREQ-----RERQLRAE-----ERQOREQFLP 830
QY 326 DQBEQEQAAGEGRNQ-----QKLRGDDYNDNEAESETDKQAALAGNDRNIDVFNVE 380
DB 831 --ESEEKQGRQRERKELOFLBEEQLQRRARAQQLQBEEDGLQEDQER-----RRQ 883
QY 381 DQKRD---TINLLDQREKRNHTL 400
DB 884 EQRDQKWRWOLEEERKERRHTL 906
RESULT 9
US-08-800-644-94
; Sequence 94, Application US/08800644
; Patent No. 5958752
; GENERAL INFORMATION:
; APPLICANT: Steinert, Peter M.
; APPLICANT: Lee, Seung-Chul
; APPLICANT: Kim, In-Gyu
; APPLICANT: Chung, Soo-Il
; APPLICANT: Park, Sang-Chul
; TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,644
; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/056,200
; FILING DATE: 30-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH054.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 760-0404
; TELEFAX: (714) 760-9502
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1898 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-800-644-94
Query Match 8.1%; Score 165; DB 2; Length 1898;
Best Local Similarity 23.2%; Pred. No. 7.3e-05;
Matches 89; Conservative 71; Mismatches 133; Indels 90; Gaps 18;
QY 49 EGRVRAAAERGAVELKKNFQGELEKQREQLDKTQSSHNFOLESVKNLYQDEKAVLVNN 108
DB 583 EQLKREQEERDQLLKREERROQLKREQEERLE--QRLKREVEERLEQEER-----634
QY 109 ITTGERLIRVLQDQ-----LKT---LQNYGRLOQDVLQFQKQNTNLERKFSYD-LSQC 158
DB 635 --RDELKREPEERERHLLKSEQEERHQLRRE--QQERROQLKREEEERLEQR 690
QY 159 INQMKVEQCEERIEEVTYKKGNEAVSR-----DLSENDRQOQLSEPPQLQAA 212
Query Match 8.1%; Score 165; DB 2; Length 1898;
Best Local Similarity 23.2%; Pred. No. 7.3e-05;
Matches 89; Conservative 71; Mismatches 133; Indels 90; Gaps 18;
QY 49 EGRVRAAAERGAVELKKNFQGELEKQREQLDKTQSSHNFOLESVKNLYQDEKAVLVNN 108
DB 583 EQLKREQEERDQLLKREERROQLKREQEERLE--QRLKREVEERLEQEER-----634
QY 109 ITTGERLIRVLQDQ-----LKT---LQNYGRLOQDVLQFQKQNTNLERKFSYD-LSQC 158
DB 635 --RDELKREPEERERHLLKSEQEERHQLRRE--QQERROQLKREEEERLEQR 690
QY 159 INQMKVEQCEERIEEVTYKKGNEAVSR-----DLSENDRQOQLSEPPQLQAA 212

DB 691 LKREHEERREQEALAEQEQAERERIKRIPKQWQLESEADARQSKVLLLEAPQ-----A 745
QY 213 GLPHTPEVPGQGNVLGNSKQTPAPSSVWLDSKQVKEETNEIQVWNEEPQRDLRPO- 271
DB 746 G--RAEAQEQ-----EKKRR-----ESELQWEEERAHFQQQEEQRRDFTWQW 789
QY 272 -----EPGRQVVDPRVGGFGAGELGQTPQVQAALSVSQENPEWEGPERDQVIP 325
DB 790 QAEKESRGRQRLSARPLREQ-----RERQLRAE-----ERQOREQFLP 830
QY 326 DQBEQEQAAGEGRNQ-----QKLRGDDYNDNEAESETDKQAALAGNDRNIDVFNVE 380
DB 831 --ESEEKQGRQRERKELOFLBEEQLQRRARAQQLQBEEDGLQEDQER-----RRQ 883
QY 381 DQKRD---TINLLDQREKRNHTL 400
DB 884 EQRDQKWRWOLEEERKERRHTL 906
RESULT 10
US-09-538-092-1280
; Sequence 1280, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurafatSeqformatter Version 0.9
; SEQ ID NO 1280
; LENGTH: 1898
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q07283
US-09-538-092-1280
Query Match 8.1%; Score 165; DB 4; Length 1898;
Best Local Similarity 23.2%; Pred. No. 7.3e-05;
Matches 89; Conservative 71; Mismatches 133; Indels 90; Gaps 18;
QY 49 EGRVRAAAERGAVELKKNFQGELEKQREQLDKTQSSHNFOLESVKNLYQDEKAVLVNN 108
DB 583 EQLKREQEERDQLLKREERROQLKREQEERLE--QRLKREVEERLEQEER-----634
QY 109 ITTGERLIRVLQDQ-----LKT---LQNYGRLOQDVLQFQKQNTNLERKFSYD-LSQC 158
DB 635 --RDELKREPEERERHLLKSEQEERHQLRRE--QQERROQLKREEEERLEQR 690
QY 159 INQMKVEQCEERIEEVTYKKGNEAVSR-----DLSENDRQOQLSEPPQLQAA 212
DB 691 LKREHEERREQEALAEQEQAERERIKRIPKQWQLESEADARQSKVLLLEAPQ-----A 745
QY 213 GLPHTPEVPGQGNVLGNSKQTPAPSSVWLDSKQVKEETNEIQVWNEEPQRDLRPO- 271
DB 746 G--RAEAQEQ-----EKKRR-----ESELQWEEERAHFQQQEEQRRDFTWQW 789
QY 272 -----EPGRQVVDPRVGGFGAGELGQTPQVQAALSVSQENPEWEGPERDQVIP 325
DB 790 QAEKESRGRQRLSARPLREQ-----RERQLRAE-----ERQOREQFLP 830
QY 326 DQBEQEQAAGEGRNQ-----QKLRGDDYNDNEAESETDKQAALAGNDRNIDVFNVE 380

[illegible]

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; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 863
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P07197
US-09-538-092-863

Query Match          7.9%; Score 160.5; DB 4; Length 915;
Best Local Similarity 19.1%; Pred. No. 6.2e-05;
Matches 87; Conservative 75; Mismatches 149; Indels 145; Gaps 17;

Qy 45 IMELEGVRRAAARGAVELKKNEFGQGELEKQREQLDKIQSHNFQLESVNKLYOD-EKA 103
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 153 IRELATLEMYNHAKAQLDSDHLEEDIHRLKRFEEEARLRDDTEAAIRALKRDIEEA 212
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 104 VLVANNITGRLIRVLQDLKTLQRYNGRLQDVL-QFKNQTNLERKFSYDLSQCINQM 162
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 213 SLVK--VELDKKVSQLDQVAFLRNHEEEVADLLAQIQASHITVERK-DYLKTDISTAL 269
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 163 KEVKEQCEE-----RIEVTKKGNEAVAS-----186
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 270 KEIRSOLESHSDQNHQAEWFKCRYAKLTEAAEQNKAIRSAKEIAFYRQLOSKSIE 329
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 187 -----RDLSENNDQROQLQ-----ALSEPQRLQA 211
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 330 LESVGTKESLERQLSDIEERHNDLSSYQDTIQLENELRGTKWEMARHLREYQDLLNV 389
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 212 AGLPHTVP-----QGK-----GNVLGN-----SKSQTPAS-----238
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 390 KMALDITIAVRYKLLGESETRFSTFAGSITGPLYTHRPPITISSIKTIQTKVEAPKLKVQH 449
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 239 ---SEVVLDSKRQVKEKETNE-IQVNNEE-----PQDRLLPOEPRGQVVEDRPVGGRG 288
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 450 KFVEEIIETKVEDEKSEMEALTAITELAA SMKKEEKEAAEKEEPEAEVEEVAAK- 508
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 289 FGGAGELGQTPQVQAALSVSQENPEMEGPERDLVDPGQEEEQE-----AAGEGRN 340
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 509 -----KSPVKA TAPVKEEKEKEEE-----QEEEEEEDEGAKSDQAEEGGS 552
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 341 QOKLRGE-DDYNNDENAESETDKQAALAGNDRNID 375
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 553 EKEGSKSEKEGEQEGETEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAE 588
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 14
US-09-949-016-6611
; Sequence 6611, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6611
; LENGTH: 916
; TYPE: PRT

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QY 104 VLVNNITTGERLIRLVQDLQKTLQRYNGRLOODVL-QFQKQNTNLERKFSYDLSQCINQM 162
Db 214 SLVK--VELDKKVSQSLQDEVAFLRSNHEEEVADLLAQIQASHITVERK-DYLKTDISTAL 270
QY 163 KEVKEQCEE-----RIEVTKKGNEAVAS----- 186
Db 271 KEIRSQLESHSDQNMHQAEWFKCRYAKLITEAAEQNKAEIRSAKEEIAEYRRQLQSKSIE 330
QY 187 -----RDLSENNDQROQLQ-----ALSEPQRLQA 211
Db 331 LESVRGTKESLERQLSDIEERHNDLSSYQDTIQOLENELRGTWKWEMARHUREYODLLNV 390
QY 212 AGLPHTVP-----QKG-----GNVLGN-----SKSQTAPS----- 238
Db 391 KMALDIEIAAYRKLEGBETRETFAGSITGPLYTHRPPTITISSKIQTKVEAPKLVQH 450
QY 239 ---SEVVLDSKRQVEKETNE-IQVNEE-----PQRDLRPOEPGREQVVEDRPVGGRG 288
Db 451 KFVEEIIIEETKVEDEKSEMEEALTAITEELAVSMKEEKEAAEKEEPEAEVEEVAAK- 509
QY 289 FGGAGELGQTPQVQAALSVSQENPEMEGPERDQLVIPDQOREEQE-----AAGEGRN 340
Db 510 -----KSPVKATAPEVKEEGEKEBEE-----QEBEEEEDEGAKSDQAEEGS 553
QY 341 OOKLRGE-DDYNMDENEAESETDKQAALAGNDRNID 375
Db 554 EKEGSSEKEEGEQEGETEAEGAEGAEEKKEKVE 589
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Search completed: June 7, 2005, 14:11:50
Job time : 46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:10:23 ; Search time 147 Seconds
(without alignments)
980.145 Million cell updates/sec

Title: US-10-759-803-2
Perfect score: 2029
Sequence: 1 MGLNGRRSMKSPPLVLAAL.....DQKRDITNLLDQREKRNHTL 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520.

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
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21: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2029	100.0	400	14	US-10-205-823-156
2	2029	100.0	400	14	US-10-177-293-184
3	2029	100.0	400	16	US-10-759-803-2
4	2029	100.0	401	10	US-09-946-374-100
5	2029	100.0	401	14	US-10-028-072-486
6	2029	100.0	401	14	US-10-140-808-486
7	2029	100.0	401	14	US-10-121-049-486
8	2029	100.0	401	14	US-10-123-904-486
9	2029	100.0	401	14	US-10-140-470-486
10	2029	100.0	401	14	US-10-175-746-486
11	2029	100.0	401	14	US-10-176-918-486
12	2029	100.0	401	14	US-10-176-921-486

13	2029	100.0	401	14	US-10-137-865-486
14	2029	100.0	401	14	US-10-140-474-486
15	2029	100.0	401	14	US-10-142-431-486
16	2029	100.0	401	14	US-10-143-114-486
17	2029	100.0	401	14	US-10-006-856A-100
18	2029	100.0	401	14	US-10-142-419-486
19	2029	100.0	401	14	US-10-123-262-486
20	2029	100.0	401	14	US-10-142-423-486
21	2029	100.0	401	14	US-10-006-818A-100
22	2029	100.0	401	14	US-10-121-050-486
23	2029	100.0	401	14	US-10-141-755-486
24	2029	100.0	401	14	US-10-143-032-486
25	2029	100.0	401	14	US-10-006-485A-100
26	2029	100.0	401	14	US-10-013-907A-100
27	2029	100.0	401	14	US-10-015-499A-100
28	2029	100.0	401	14	US-10-123-108-486
29	2029	100.0	401	14	US-10-123-236-486
30	2029	100.0	401	14	US-10-123-261-486
31	2029	100.0	401	14	US-10-140-921-486
32	2029	100.0	401	14	US-10-142-423-486
33	2029	100.0	401	14	US-10-015-393A-100
34	2029	100.0	401	14	US-10-015-869A-100
35	2029	100.0	401	14	US-10-121-045-486
36	2029	100.0	401	14	US-10-123-292-486
37	2029	100.0	401	14	US-10-123-903-486
38	2029	100.0	401	14	US-10-124-819-486
39	2029	100.0	401	14	US-10-124-822-486
40	2029	100.0	401	14	US-10-140-925-486
41	2029	100.0	401	14	US-10-160-498-486
42	2029	100.0	401	14	US-10-012-121A-100
43	2029	100.0	401	14	US-10-124-824-486
44	2029	100.0	401	14	US-10-127-825A-486
45	2029	100.0	401	14	US-10-127-829A-486

ALIGNMENTS

RESULT 1

US-10-205-823-156
; Sequence 156, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsley, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156

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; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-156

Query Match      100.0%; Score 2029; DB 14; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MGLNGRSMKSPPLVLAALVACIIIVLGFNTWIASRSVDLQTRIMELEGRVRRAAARG 60

Qy 61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVNKLYODEKAVLVNNTTGERLIRVLQ 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVNKLYODEKAVLVNNTTGERLIRVLQ 120

Qy 121 DQKTLQRYNRLQDVLQFQKQNTNLERKFSYDLSQCINOMKEVKEQCEERIEVTKKG 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 DQKTLQRYNRLQDVLQFQKQNTNLERKFSYDLSQCINOMKEVKEQCEERIEVTKKG 180

Qy 181 NEAVASRLSENNDORQQLALSEPQRLQAAGLPHTVEPQKGNVLGNSKSTPAPSS 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 NEAVASRLSENNDORQQLALSEPQRLQAAGLPHTVEPQKGNVLGNSKSTPAPSS 240

Qy 241 VVLDKRVQVEKEETNEIOVNNEEPORDRLPOEPGREQVVEDRPVCGRGFGGAGELGQTPQ 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 VVLDKRVQVEKEETNEIOVNNEEPORDRLPOEPGREQVVEDRPVCGRGFGGAGELGQTPQ 300

Qy 301 VQAAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGEDDYNNDENEAS 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 VQAAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGEDDYNNDENEAS 360

Qy 361 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNTL 400
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
361 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNTL 400

RESULT 2
US-10-177-293-184
; Sequence 184, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastien
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jk., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
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; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-184

Query Match      100.0%; Score 2029; DB 14; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLNGRSMKSPPLVLAALVACIIIVLGFNTWIASRSVDLQTRIMELEGRVRRAAARG 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MGLNGRSMKSPPLVLAALVACIIIVLGFNTWIASRSVDLQTRIMELEGRVRRAAARG 60

Qy 61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVNKLYODEKAVLVNNTTGERLIRVLQ 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVNKLYODEKAVLVNNTTGERLIRVLQ 120

Qy 121 DQKTLQRYNRLQDVLQFQKQNTNLERKFSYDLSQCINOMKEVKEQCEERIEVTKKG 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 DQKTLQRYNRLQDVLQFQKQNTNLERKFSYDLSQCINOMKEVKEQCEERIEVTKKG 180

Qy 181 NEAVASRLSENNDORQQLALSEPQRLQAAGLPHTVEPQKGNVLGNSKSTPAPSS 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 NEAVASRLSENNDORQQLALSEPQRLQAAGLPHTVEPQKGNVLGNSKSTPAPSS 240

Qy 241 VVLDKRVQVEKEETNEIOVNNEEPORDRLPOEPGREQVVEDRPVCGRGFGGAGELGQTPQ 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 VVLDKRVQVEKEETNEIOVNNEEPORDRLPOEPGREQVVEDRPVCGRGFGGAGELGQTPQ 300

Qy 301 VQAAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGEDDYNNDENEAS 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 VQAAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGEDDYNNDENEAS 360

Qy 361 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNTL 400
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
361 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNTL 400

RESULT 3
US-10-759-803-2
; Sequence 2, Application US/10759803
; Publication No. US20040265310A1
; GENERAL INFORMATION:
; APPLICANT: AFAR, Daniel E. H.
; APPLICANT: HUBERT, Rene S.
; APPLICANT: LEONG, Kahan
; APPLICANT: RAITANO, Arthur B.
; APPLICANT: SAPPAN, Douglas C.
; TITLE OF INVENTION: NOVEL PROSTATE-RESTRICTED GENE EXPRESSED
; FILE REFERENCE: 129.13USUI
; CURRENT APPLICATION NUMBER: US/10/759,803
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US/09/547,788
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/128,860
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: SIGNAL
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; LOCATION: (1)....(29)
US-10-759-803-2
Query Match      100.0%; Score 2029; DB 16; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLGNRSMKSPPIVLAAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRAAABRG 60
Db 1 MGLGNRSMKSPPIVLAAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRAAABRG 60
QY 61 AVELKKNFQGELEKQREOLDKIQSHNFQLESVKNLYODEKAVLVNNTTGERLIRVLQ 120
Db 61 AVELKKNFQGELEKQREOLDKIQSHNFQLESVKNLYODEKAVLVNNTTGERLIRVLQ 120
QY 121 DQLKTLQRYNGLQDVLQFQKQNTLNLERKSYDLSQICINOMKEVKEQCEERIEBVTKKG 180
Db 121 DQLKTLQRYNGLQDVLQFQKQNTLNLERKSYDLSQICINOMKEVKEQCEERIEBVTKKG 180
QY 181 NEAVASRLSENNDQRLQALSEPQRLQAAGLPHTPEVPOQKGNVLGNSKSTQTPAPSE 240
Db 181 NEAVASRLSENNDQRLQALSEPQRLQAAGLPHTPEVPOQKGNVLGNSKSTQTPAPSE 240
QY 241 VVLDKQVKEEETNEIQVNEEPQDRDLPOEPGREQVVEDRPGRGFGGAGELGQTPQ 300
Db 241 VVLDKQVKEEETNEIQVNEEPQDRDLPOEPGREQVVEDRPGRGFGGAGELGQTPQ 300
QY 301 VOALSVSQENPEMGPEDQDLVDPGQEEQEAAGEGRNQKLGEDDYNNDENAESE 360
Db 301 VOALSVSQENPEMGPEDQDLVDPGQEEQEAAGEGRNQKLGEDDYNNDENAESE 360
QY 361 TDKQAALAGNRNDIDFVNVEDQKRTINLLDQREKRNHTL 400
Db 361 TDKQAALAGNRNDIDFVNVEDQKRTINLLDQREKRNHTL 400

RESULT 4
US-09-946-374-100
; Sequence 100, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC1
; CURRENT APPLICATION NUMBER: US/09/946.374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100390
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; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
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; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
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; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
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; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
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; PRIOR APPLICATION NUMBER: 60/103401
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; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08

; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 2029; DB 10; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131; Mismatches 0; Indels 0; Gaps 0;
Matches 400; Conservative 0;

Qy 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNTYWIASSRSDVLQTRIMELEGRVRRAAERG 60
Db 2 MGLNGRRSMKSPPLVLAALVACIIVLGFNTYWIASSRSDVLQTRIMELEGRVRRAAERG 61

Qy 61 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNNKLYQDEKAVLVNNITTTGERLIRVLQ 120
Db 62 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNNKLYQDEKAVLVNNITTTGERLIRVLQ 121

Qy 121 DOLKTLQRYNGLQODVLQFQKQNTNLERKESYDLQSCINOMKEVKEOCEERIEBVTKKG 180
Db 122 DOLKTLQRYNGLQODVLQFQKQNTNLERKESYDLQSCINOMKEVKEOCEERIEBVTKKG 181

Qy 181 NEAVASRDLSNNQDQQLQALSEPPQRLQAGLPHTPEVPOQKGNVLGNSKSTPAPSE 240
Db 182 NEAVASRDLSNNQDQQLQALSEPPQRLQAGLPHTPEVPOQKGNVLGNSKSTPAPSE 241

Qy 241 VVLSKQKQVEKEETNEIOVNVNEEPQDRLPQEPQREQVVEDRVPVGGRGFGGAGELGQTPQ 300
Db 242 VVLSKQKQVEKEETNEIOVNVNEEPQDRLPQEPQREQVVEDRVPVGGRGFGGAGELGQTPQ 301

Qy 301 VQAALSVSOENPEMPEGPERDQVLPDGOEERQEAAGEGRNOQKLRGEDDYNDENEASE 360
Db 302 VQAALSVSOENPEMPEGPERDQVLPDGOEERQEAAGEGRNOQKLRGEDDYNDENEASE 361

Qy 361 TDKQALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400
Db 362 TDKQALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 401

RESULT 5
US-10-028-072-486
; Sequence 486, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deanoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063704
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063733
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; PRIOR FILING DATE: 1997-10-29
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; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/065846
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 60/073612
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
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; PRIOR FILING DATE: 1998-05-22

; PRIOR APPLICATION NUMBER: 60/087106
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 ; PRIOR FILING DATE: 1998-06-23
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 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/091360
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07

Query Match 100.0%; Score 2029; DB 14; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2.9e-131;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRAAABRG 60
 DB 2 MGLNGRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRAAABRG 61
 QY 61 AVELKKNBFQGELEKQREQLDKIQSSHNFQLESVNKLYODEKAVLVNNITTTGERLIRVLQ 120
 DB 62 AVELKKNBFQGELEKQREQLDKIQSSHNFQLESVNKLYODEKAVLVNNITTTGERLIRVLQ 121
 QY 121 DOLKTLQRYNGRLQODVLQFQKQNTNLERKFSYDLSCINQMKVEKCEERIEEVTKKG 180
 DB 122 DOLKTLQRYNGRLQODVLQFQKQNTNLERKFSYDLSCINQMKVEKCEERIEEVTKKG 181
 QY 181 NEAVASRLSENNDORQQLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 240
 DB 182 NEAVASRLSENNDORQQLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 241
 QY 241 VVLDKSRQVEKETNEIQVNEEPQRLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 300
 DB 242 VVLDKSRQVEKETNEIQVNEEPQRLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 301
 QY 301 VVLDKSRQVEKETNEIQVNEEPQRLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 360
 DB 302 VVLDKSRQVEKETNEIQVNEEPQRLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 361
 QY 361 TDQQAALAGNDRNIDVFNVEDQKRTDINLLDQREKRNHTL 400
 DB 362 TDQQAALAGNDRNIDVFNVEDQKRTDINLLDQREKRNHTL 401

RESULT 6
 US-10-140-808-486
 ; Sequence 486, Application US/10140808

; Publication No. US20030017563A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3330R1C182
 ; CURRENT APPLICATION NUMBER: US/10/140,808
 ; CURRENT FILING DATE: 2002-05-07
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 486
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-140-808-486

Query Match 100.0%; Score 2029; DB 14; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2.9e-131;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRAAABRG 60
 DB 2 MGLNGRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRAAABRG 61
 QY 61 AVELKKNBFQGELEKQREQLDKIQSSHNFQLESVNKLYODEKAVLVNNITTTGERLIRVLQ 120
 DB 62 AVELKKNBFQGELEKQREQLDKIQSSHNFQLESVNKLYODEKAVLVNNITTTGERLIRVLQ 121
 QY 121 DOLKTLQRYNGRLQODVLQFQKQNTNLERKFSYDLSCINQMKVEKCEERIEEVTKKG 180
 DB 122 DOLKTLQRYNGRLQODVLQFQKQNTNLERKFSYDLSCINQMKVEKCEERIEEVTKKG 181
 QY 181 NEAVASRLSENNDORQQLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 240
 DB 182 NEAVASRLSENNDORQQLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 241
 QY 241 VVLDKSRQVEKETNEIQVNEEPQRLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 300
 DB 242 VVLDKSRQVEKETNEIQVNEEPQRLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 301
 QY 301 VVLDKSRQVEKETNEIQVNEEPQRLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 360
 DB 302 VVLDKSRQVEKETNEIQVNEEPQRLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 361
 QY 361 TDQQAALAGNDRNIDVFNVEDQKRTDINLLDQREKRNHTL 400
 DB 362 TDQQAALAGNDRNIDVFNVEDQKRTDINLLDQREKRNHTL 401

RESULT 7
 US-10-121-049-486
 ; Sequence 486, Application US/10121049
 ; Publication No. US20030022239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura

```

; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 486
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-486

Query Match      100.0%; Score 2029; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 60
Db 2 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 61

Qy 61 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ 120
Db 62 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ 121

Qy 121 DQKTLQRYNRLQDVLQFQKQNTNLERKFSYDLSCINOMKEVKEOCEERIEVTKKG 180
Db 122 DQKTLQRYNRLQDVLQFQKQNTNLERKFSYDLSCINOMKEVKEOCEERIEVTKKG 181

Qy 181 NEAVASRLSENDRQQLQALSEPQRLQAAGLPHTPEVPGKGNVLSKSTQTPAPSE 240
Db 182 NEAVASRLSENDRQQLQALSEPQRLQAAGLPHTPEVPGKGNVLSKSTQTPAPSE 241

Qy 241 VVLSKQVKEETNEIQVNEEPQDRDLQPEPGREQVVEDRPGVGRFGGAGELGQTPQ 300
Db 242 VVLSKQVKEETNEIQVNEEPQDRDLQPEPGREQVVEDRPGVGRFGGAGELGQTPQ 301

Qy 301 VQAAALSVQENPEMGPEDQVLPDGOEEQEAAGEGNOCKLGEDDYNDENEAESE 360
Db 302 VQAAALSVQENPEMGPEDQVLPDGOEEQEAAGEGNOCKLGEDDYNDENEAESE 361

Qy 361 TDQAALAGNDRNIDVFNVEDQKRTDINLLDQREKRNHTL 400
Db 362 TDQAALAGNDRNIDVFNVEDQKRTDINLLDQREKRNHTL 401

RESULT 8
US-10-123-904-486
; Sequence 486, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Goddard, Audrey

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; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 486
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-486

Query Match      100.0%; Score 2029; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 60
Db 2 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 61

Qy 61 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ 120
Db 62 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ 121

Qy 121 DQKTLQRYNRLQDVLQFQKQNTNLERKFSYDLSCINOMKEVKEOCEERIEVTKKG 180
Db 122 DQKTLQRYNRLQDVLQFQKQNTNLERKFSYDLSCINOMKEVKEOCEERIEVTKKG 181

Qy 181 NEAVASRLSENDRQQLQALSEPQRLQAAGLPHTPEVPGKGNVLSKSTQTPAPSE 240
Db 182 NEAVASRLSENDRQQLQALSEPQRLQAAGLPHTPEVPGKGNVLSKSTQTPAPSE 241

Qy 241 VVLSKQVKEETNEIQVNEEPQDRDLQPEPGREQVVEDRPGVGRFGGAGELGQTPQ 300
Db 242 VVLSKQVKEETNEIQVNEEPQDRDLQPEPGREQVVEDRPGVGRFGGAGELGQTPQ 301

Qy 301 VQAAALSVQENPEMGPEDQVLPDGOEEQEAAGEGNOCKLGEDDYNDENEAESE 360
Db 302 VQAAALSVQENPEMGPEDQVLPDGOEEQEAAGEGNOCKLGEDDYNDENEAESE 361

Qy 361 TDQAALAGNDRNIDVFNVEDQKRTDINLLDQREKRNHTL 400
Db 362 TDQAALAGNDRNIDVFNVEDQKRTDINLLDQREKRNHTL 401

RESULT 9
US-10-140-470-486
; Sequence 486, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.

```

```
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 486
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-486

Query Match      100.0%; Score 2029; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNTWIASRSVDLQTRIMELEGRVRRRAAERG 60
Db 2 MGLNGRRSMKSPPLVLAALVACIIVLGFNTWIASRSVDLQTRIMELEGRVRRRAAERG 61
QY 61 AVELKKNFQGELEKQREOLDKIOSSHNFQLESVNKLYQDEKAVLVNNTTGERLIRVLQ 120
Db 62 AVELKKNFQGELEKQREOLDKIOSSHNFQLESVNKLYQDEKAVLVNNTTGERLIRVLQ 121
QY 121 DQLKTLQRYNRLQODVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEBVTKKG 180
Db 122 DQLKTLQRYNRLQODVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEBVTKKG 181
QY 181 NEAVASRLSENNDORQOLQALSEPQRLQAGLPHTVEVPQKGNVLGNSKSTQTPAPSE 240
Db 182 NEAVASRLSENNDORQOLQALSEPQRLQAGLPHTVEVPQKGNVLGNSKSTQTPAPSE 241
QY 241 VVLSKQVKEETNEIQVNNEEPQDRLPQPGREQVVEDRPGVGRFGGAGELGQTPQ 300
Db 242 VVLSKQVKEETNEIQVNNEEPQDRLPQPGREQVVEDRPGVGRFGGAGELGQTPQ 301
QY 301 VQAALSVSQENPEMGPEDQLVIPDGQEEQEAAGEGRNQKLRGDDYNNDENEARSE 360
Db 302 VQAALSVSQENPEMGPEDQLVIPDGQEEQEAAGEGRNQKLRGDDYNNDENEARSE 361
QY 361 TDQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400
Db 362 TDQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 401
```

```
RESULT 10
US-10-175-746-486
; Sequence 486, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

```
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 486
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-486

Query Match      100.0%; Score 2029; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNTWIASRSVDLQTRIMELEGRVRRRAAERG 60
Db 2 MGLNGRRSMKSPPLVLAALVACIIVLGFNTWIASRSVDLQTRIMELEGRVRRRAAERG 61
QY 61 AVELKKNFQGELEKQREOLDKIOSSHNFQLESVNKLYQDEKAVLVNNTTGERLIRVLQ 120
Db 62 AVELKKNFQGELEKQREOLDKIOSSHNFQLESVNKLYQDEKAVLVNNTTGERLIRVLQ 121
QY 121 DQLKTLQRYNRLQODVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEBVTKKG 180
Db 122 DQLKTLQRYNRLQODVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEBVTKKG 181
QY 181 NEAVASRLSENNDORQOLQALSEPQRLQAGLPHTVEVPQKGNVLGNSKSTQTPAPSE 240
Db 182 NEAVASRLSENNDORQOLQALSEPQRLQAGLPHTVEVPQKGNVLGNSKSTQTPAPSE 241
QY 241 VVLSKQVKEETNEIQVNNEEPQDRLPQPGREQVVEDRPGVGRFGGAGELGQTPQ 300
Db 242 VVLSKQVKEETNEIQVNNEEPQDRLPQPGREQVVEDRPGVGRFGGAGELGQTPQ 301
QY 301 VQAALSVSQENPEMGPEDQLVIPDGQEEQEAAGEGRNQKLRGDDYNNDENEARSE 360
Db 302 VQAALSVSQENPEMGPEDQLVIPDGQEEQEAAGEGRNQKLRGDDYNNDENEARSE 361
QY 361 TDQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400
Db 362 TDQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 401
```

```
RESULT 11
US-10-176-918-486
; Sequence 486, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
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; NUMBER OF SEQ ID NOS: 550		Query Match		100.0%; Score 2029; DB 14; Length 401;	
; SEQ ID NO 486		Best Local Similarity		100.0%; Pred. No. 2.9e-131;	
; LENGTH: 401		Matches 400; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
; TYPE: PRT		; ORGANISM: Homo Sapien			
US-10-176-918-486					
QY	1	MGLNGRSMKSPPLVLAALVACIIIVLGNFYWIASRSVDLQTRIMELEGRVRRAAERG	60		
DB	2	MGLNGRSMKSPPLVLAALVACIIIVLGNFYWIASRSVDLQTRIMELEGRVRRAAERG	61		
QY	61	AVELKKNFQGELEKQREQLDKIQSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ	120		
DB	62	AVELKKNFQGELEKQREQLDKIQSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ	121		
QY	121	DQLKTLQRYNGLQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEBVTGG	180		
DB	122	DQLKTLQRYNGLQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEBVTGG	181		
QY	181	NEAVASRDLSENNDORQQLQALSEPQRLQAGLPHTPEVPGKGVLGNSKSTQTPAPSE	240		
DB	182	NEAVASRDLSENNDORQQLQALSEPQRLQAGLPHTPEVPGKGVLGNSKSTQTPAPSE	241		
QY	241	VVLDSKROVEKEETNEIOVNEEPORDRLPOBPGREQVVEDRPGRGFGGAGELGQTPQ	300		
DB	242	VVLDSKROVEKEETNEIOVNEEPORDRLPOBPGREQVVEDRPGRGFGGAGELGQTPQ	301		
QY	301	VOAALSVSQENPEMGPEDQLVIPDGOEEQEAAGEGRNQOKLRGDDYNNDENEASE	360		
DB	302	VOAALSVSQENPEMGPEDQLVIPDGOEEQEAAGEGRNQOKLRGDDYNNDENEASE	361		
QY	361	TDKQALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL	400		
DB	362	TDKQALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL	401		
RESULT 12					
US-10-176-921-486		Query Match		100.0%; Score 2029; DB 14; Length 401;	
; Sequence 486, Application US/10176921		Best Local Similarity		100.0%; Pred. No. 2.9e-131;	
; Publication No. US20030027276A1		Matches 400; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
; GENERAL INFORMATION:		; ORGANISM: Homo Sapien			
; APPLICANT: Baker, Kevin P.					
; APPLICANT: Beresini, Maureen					
; APPLICANT: Deforge, Laura					
; APPLICANT: Desnoyers, Luc					
; APPLICANT: Filvaroff, Ellen					
; APPLICANT: Gao, Wei-Qiang					
; APPLICANT: Gerritsen, Mary E.					
; APPLICANT: Goddard, Audrey					
; APPLICANT: Godowski, Paul J.					
; APPLICANT: Gurney, Austin L.					
; APPLICANT: Sherwood, Steven					
; APPLICANT: Smith, Victoria					
; APPLICANT: Stewart, Timothy A.					
; APPLICANT: Tumas, Daniel					
; APPLICANT: Watanabe, Colin K					
; APPLICANT: Wood, William					
; APPLICANT: Zhang, Zemin					
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC					
; FILE REFERENCE: P3330RLC288					
; CURRENT APPLICATION NUMBER: US/10/176,921					
; CURRENT FILING DATE: 2002-06-20					
; Prior Application removed - See File Wrapper or Palm					
; NUMBER OF SEQ ID NOS: 550					
; SEQ ID NO 486					
; LENGTH: 401					
; TYPE: PRT					
; ORGANISM: Homo Sapien					
US-10-176-921-486					
QY	1	MGLNGRSMKSPPLVLAALVACIIIVLGNFYWIASRSVDLQTRIMELEGRVRRAAERG	60		
DB	2	MGLNGRSMKSPPLVLAALVACIIIVLGNFYWIASRSVDLQTRIMELEGRVRRAAERG	61		
QY	61	AVELKKNFQGELEKQREQLDKIQSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ	120		
DB	62	AVELKKNFQGELEKQREQLDKIQSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ	121		
QY	121	DQLKTLQRYNGLQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEBVTGG	180		
DB	122	DQLKTLQRYNGLQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEBVTGG	181		
QY	181	NEAVASRDLSENNDORQQLQALSEPQRLQAGLPHTPEVPGKGVLGNSKSTQTPAPSE	240		
DB	182	NEAVASRDLSENNDORQQLQALSEPQRLQAGLPHTPEVPGKGVLGNSKSTQTPAPSE	241		
QY	241	VVLDSKROVEKEETNEIOVNEEPORDRLPOBPGREQVVEDRPGRGFGGAGELGQTPQ	300		
DB	242	VVLDSKROVEKEETNEIOVNEEPORDRLPOBPGREQVVEDRPGRGFGGAGELGQTPQ	301		
QY	301	VOAALSVSQENPEMGPEDQLVIPDGOEEQEAAGEGRNQOKLRGDDYNNDENEASE	360		
DB	302	VOAALSVSQENPEMGPEDQLVIPDGOEEQEAAGEGRNQOKLRGDDYNNDENEASE	361		
QY	361	TDKQALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL	400		
DB	362	TDKQALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL	401		
RESULT 13					
US-10-137-865-486		Query Match		100.0%; Score 2029; DB 14; Length 401;	
; Sequence 486, Application US/10137865		Best Local Similarity		100.0%; Pred. No. 2.9e-131;	
; Publication No. US20030032155A1		Matches 400; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
; GENERAL INFORMATION:		; ORGANISM: Homo Sapien			
; APPLICANT: Baker, Kevin P.					
; APPLICANT: Beresini, Maureen					
; APPLICANT: Deforge, Laura					
; APPLICANT: Desnoyers, Luc					
; APPLICANT: Filvaroff, Ellen					
; APPLICANT: Gao, Wei-Qiang					
; APPLICANT: Gerritsen, Mary E.					
; APPLICANT: Goddard, Audrey					
; APPLICANT: Godowski, Paul J.					
; APPLICANT: Gurney, Austin L.					
; APPLICANT: Sherwood, Steven					
; APPLICANT: Smith, Victoria					
; APPLICANT: Stewart, Timothy A.					
; APPLICANT: Tumas, Daniel					
; APPLICANT: Watanabe, Colin K					
; APPLICANT: Wood, William					
; APPLICANT: Zhang, Zemin					
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC					
; FILE REFERENCE: P3330RLC154					
; CURRENT APPLICATION NUMBER: US/10/137,865					
; CURRENT FILING DATE: 2002-05-03					
; Prior Application removed - See Palm or File Wrapper					
; NUMBER OF SEQ ID NOS: 550					
; SEQ ID NO 486					
; LENGTH: 401					
; TYPE: PRT					
; ORGANISM: Homo Sapien					
US-10-137-865-486					

Qy 1 MGLNGRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRAAARG 60
 Db 2 MGLNGRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRAAARG 61
 Qy 61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNNITTTGERLIRVLQ 120
 Db 62 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNNITTTGERLIRVLQ 121
 Qy 121 DQKTLQRYNRLQODVLQFQKQNTNLERKFSYDLSCINOMKEVKEQCEERIEEVTYKG 180
 Db 122 DQKTLQRYNRLQODVLQFQKQNTNLERKFSYDLSCINOMKEVKEQCEERIEEVTYKG 181
 Qy 181 NEAVASRDLSNNDRQOLQALSEPOPLQAGLPHTTEVPOGKGNVLSKSTQTPAPSE 240
 Db 182 NEAVASRDLSNNDRQOLQALSEPOPLQAGLPHTTEVPOGKGNVLSKSTQTPAPSE 241
 Qy 241 VVLDSKQVEKEETNEIQVNEEPQDRDLPOEPGREQVVEDRPGGRGFGGAGELGQTPQ 300
 Db 242 VVLDSKQVEKEETNEIQVNEEPQDRDLPOEPGREQVVEDRPGGRGFGGAGELGQTPQ 301
 Qy 301 VQAAALSVSQENPEMGPGRDQVLPDQGEHEQEAAGEGRNQKLRGDDYNNDENEAESE 360
 Db 302 VQAAALSVSQENPEMGPGRDQVLPDQGEHEQEAAGEGRNQKLRGDDYNNDENEAESE 361
 Qy 361 TDQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 400
 Db 362 TDQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 401

RESULT 14

US-10-140-474-486
 ; Sequence 486, Application US/10140474
 ; Publication No. US20030032156A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tamas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330R1C162
 ; CURRENT APPLICATION NUMBER: US/10/140,474
 ; CURRENT FILING DATE: 2002-05-06
 ; Prior Application removed - See Palm or File Wrapper
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 486
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-140-474-486

Query Match 100.0%; Score 2029; DB 14; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2.9e-131;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGLNGRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRAAARG 60
 Db 2 MGLNGRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRAAARG 61

Qy 61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNNITTTGERLIRVLQ 120
 Db 62 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNNITTTGERLIRVLQ 121
 Qy 121 DQKTLQRYNRLQODVLQFQKQNTNLERKFSYDLSCINOMKEVKEQCEERIEEVTYKG 180
 Db 122 DQKTLQRYNRLQODVLQFQKQNTNLERKFSYDLSCINOMKEVKEQCEERIEEVTYKG 181
 Qy 181 NEAVASRDLSNNDRQOLQALSEPOPLQAGLPHTTEVPOGKGNVLSKSTQTPAPSE 240
 Db 182 NEAVASRDLSNNDRQOLQALSEPOPLQAGLPHTTEVPOGKGNVLSKSTQTPAPSE 241
 Qy 241 VVLDSKQVEKEETNEIQVNEEPQDRDLPOEPGREQVVEDRPGGRGFGGAGELGQTPQ 300
 Db 242 VVLDSKQVEKEETNEIQVNEEPQDRDLPOEPGREQVVEDRPGGRGFGGAGELGQTPQ 301
 Qy 301 VQAAALSVSQENPEMGPGRDQVLPDQGEHEQEAAGEGRNQKLRGDDYNNDENEAESE 360
 Db 302 VQAAALSVSQENPEMGPGRDQVLPDQGEHEQEAAGEGRNQKLRGDDYNNDENEAESE 361
 Qy 361 TDQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 400
 Db 362 TDQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 401

RESULT 15

US-10-142-431-486
 ; Sequence 486, Application US/10142431
 ; Publication No. US20030036179A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tamas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330R1C251
 ; CURRENT APPLICATION NUMBER: US/10/142,431
 ; CURRENT FILING DATE: 2002-05-10
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 486
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-142-431-486

Query Match 100.0%; Score 2029; DB 14; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2.9e-131;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGLNGRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRAAARG 60
 Db 2 MGLNGRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRAAARG 61
 Qy 61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNNITTTGERLIRVLQ 120
 Db 62 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNNITTTGERLIRVLQ 121
 Qy 121 DQKTLQRYNRLQODVLQFQKQNTNLERKFSYDLSCINOMKEVKEQCEERIEEVTYKG 180

||||| 122 DQKTLQRYNRLQDDVLQFQKNQTNLERKFSYDLSQCINQMKVKEQCEERIEVTKKG 181
QY 181 NEAVASRDLSENNDORQQLQALSEPQRLQAAGLPHTTEVPQKGNVLGNSKSKQTPAPSSSE 240
Db 182 NEAVASRDLSENNDORQQLQALSEPQRLQAAGLPHTTEVPQKGNVLGNSKSKQTPAPSSSE 241
QY 241 VVLDKSRQVKEKETNEIQVNEEPORDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
Db 242 VVLDKSRQVKEKETNEIQVNEEPORDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQ 301
QY 301 VQAALSVSQENPEMEGPERDQLVIFDGOEEEOEAAAGEGRNQKLRGEDDYNNMDENEAESE 360
Db 302 VQAALSVSQENPEMEGPERDQLVIFDGOEEEOEAAAGEGRNQKLRGEDDYNNMDENEAESE 361
QY 361 TDKQALAGNDRNIDVFNVEDQKRTIINLLDQREKRNHTL 400
Db 362 TDKQALAGNDRNIDVFNVEDQKRTIINLLDQREKRNHTL 401

Search completed: June 7, 2005, 14:23:40
Job time : 149 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 13:57:30 ; Search time 162 Seconds
(without alignments)
954.964 Million cell updates/sec

Title: US-10-759-803-2

Perfect score: 2029

Sequence: 1 MGLNGRRSMKSPPLVLAAL.....DQKRDITNLLDQREKRNHTL 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2029	100.0	400	3	AAB24352 Human pro
2	2029	100.0	400	6	ABR47475 Breast ca
3	2029	100.0	400	7	ADB75332 Prostate
4	2029	100.0	401	3	AAY99368 Human PRO
5	2029	100.0	401	4	AAB66117 Protein o
6	2029	100.0	401	4	AAU12414 Human PRO
7	2029	100.0	401	4	AAB49770 Amyloid-b
8	2029	100.0	401	4	AAB93295 Human pro
9	2029	100.0	401	4	ABR88480 Human mem
10	2029	100.0	401	5	ABP65020 Human pro
11	2029	100.0	401	6	ABO17858 Novel hum
12	2029	100.0	401	6	ABU81112 Human PRO
13	2029	100.0	401	6	ABU66812 Human PRO
14	2029	100.0	401	6	ABU59893 Novel sec
15	2029	100.0	401	6	ABO25083 Human sec
16	2029	100.0	401	6	ABU67088 Human sec
17	2029	100.0	401	6	ADA46005 Novel hum
18	2029	100.0	401	6	ADA76436 Human PRO
19	2029	100.0	401	6	ADA19086 Human PRO
20	2029	100.0	401	6	ADA61709 Homo sapi
21	2029	100.0	401	6	ADB19494 Novel hum
22	2029	100.0	401	6	ADB28035 Human PRO
23	2029	100.0	401	6	ADA86514 Novel hum
24	2029	100.0	401	6	ADB16078 Human PRO
25	2029	100.0	401	6	ADA47864 Human PRO

26	2029	100.0	401	6	ABO33610 Novel hum
27	2029	100.0	401	6	ADA67659 Human PRO
28	2029	100.0	401	6	ADB30666 Human PRO
29	2029	100.0	401	6	ADA85962 Novel hum
30	2029	100.0	401	6	ADA97174 Human PRO
31	2029	100.0	401	6	ADA79478 Human PRO
32	2029	100.0	401	6	ADA87617 Novel hum
33	2029	100.0	401	6	ADB16819 Human PRO
34	2029	100.0	401	6	ADA91911 Novel hum
35	2029	100.0	401	6	ADB14974 Human PRO
36	2029	100.0	401	6	ADB18935 Novel hum
37	2029	100.0	401	6	ADA94150 Human PRO
38	2029	100.0	401	6	ADB20046 Novel hum
39	2029	100.0	401	6	ADB13358 Human PRO
40	2029	100.0	401	6	ABO43391 Novel hum
41	2029	100.0	401	6	ADA74612 Human PRO
42	2029	100.0	401	6	ADB24845 Human PRO
43	2029	100.0	401	6	ADA82369 Human PRO
44	2029	100.0	401	6	ADA75332 Human PRO
45	2029	100.0	401	6	ADA85410 Novel hum

ALIGNMENTS

RESULT 1

AAB24352

ID AAB24352 standard; protein; 400 AA.

XX AC AAB24352;

DT 14-FEB-2001 (first entry)

DE Human prostate specific 30P3C8 protein sequence SEQ ID NO:2.

KW Human; prostate specific gene; 30P3C8; prostate cancer; diagnosis;

KW cytostatic; gene therapy; vaccine; tumour.

OS Homo sapiens.

PN WO200061610-A2.

XX PD 19-OCT-2000.

PF 12-APR-2000; 2000WO-US010218.

XX PR 12-APR-1999; 99US-0128860P.

XX PA (UROG-) UROGENESYS INC.

PI Afar DE, Hubert RS, Leong K, Raitano AB, Saffran DC;

DR WPI; 2000-619224/59.

XX DR N-FSDB; AAC64559.

PT 30P3C8 polypeptide and polynucleotide used for diagnosing, treating and monitoring development of prostate cancer.

PS Claim 1; Page 94-95; 99pp; English.

CC The present sequence is the human prostate specific protein 30P3C8, which is over-expressed in prostate cancer cells. 30P3C8 has cytostatic activity and can be used in vaccines and gene therapy. Methods for detecting the levels of 30P3C8 protein or mRNA in prostate tissue, bone tissue, lymphatic tissue, serum, blood or semen are used for diagnosing the presence of cancer in an individual or dysregulated cell growth e.g. hyperplasia. The cancers which are detected or diagnosed are of the bladder, pancreas, colon, brain, bone, lung, kidney or prostate by using test samples of serum, blood or urine or tissues of the bladder, pancreas, colon, brain, bone, lung, kidney and prostate. 30P3C8 polynucleotide sequences can be used for treating cancers expressing 30P3C8, particularly prostate cancers. Immunogenic portions of 30P3C8 are used in vaccines to inhibit the development of cancer. Anti-30P3C8

CC monoclonal antibodies bind to 30P3C8 and disrupt interactions between
CC 30P3C8 and other proteins e.g. receptors for which 30P3C8 is a ligand.
CC 30P3C8 may be a growth factor or other molecules involved in tumour growth
CC and metastasis and so anti-30P3C8 antibodies may disrupt the homing or
CC invasion or other cancer promoting activities of 30P3C8. The assays are
CC used for detecting, staging and monitoring prostate cancer. The 30P3C8
CC protein or mRNA are used as additional specific markers for detecting
CC prostate cancer and provide a more specific assay than the serum prostate
CC specific antigen (PSA) assay
XX
SQ Sequence 400 AA;

Query Match 100.0%; Score 2029; DB 3; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLGNGRRSMKSPPLVLAALVACIIIVLGFNWYIASSRSVDLQTRIMELEGRVRRAAERG 60
Db 1 MGLGNGRRSMKSPPLVLAALVACIIIVLGFNWYIASSRSVDLQTRIMELEGRVRRAAERG 60
QY 61 AVELKKNFQGELEKQREOLDKIOSHNFOLESVNKL YODEKAVLVNNITTTGERLIRVLQ 120
Db 61 AVELKKNFQGELEKQREOLDKIOSHNFOLESVNKL YODEKAVLVNNITTTGERLIRVLQ 120
QY 121 DOLKTLQRYNGLQODVLQFQKNQTNLERKFSYDLSQCINQMKVKEQCEERIEBVTKKG 180
Db 121 DOLKTLQRYNGLQODVLQFQKNQTNLERKFSYDLSQCINQMKVKEQCEERIEBVTKKG 180
QY 181 NEAVASRDLSNNDRQQLQALSEPQPRLOAAGLPHTPEVPOQKGNVLGNSKSTQTPAPSE 240
Db 181 NEAVASRDLSNNDRQQLQALSEPQPRLOAAGLPHTPEVPOQKGNVLGNSKSTQTPAPSE 240
QY 241 VVLDKSRQVKEETNEIQVNNEEPQDRDLPOEPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
Db 241 VVLDKSRQVKEETNEIQVNNEEPQDRDLPOEPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
QY 301 VOAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGEGDDYNNDENEASE 360
Db 301 VOAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGEGDDYNNDENEASE 360
QY 361 TDKQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400
Db 361 TDKQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400

RESULT 2
ABR47475
ID ABR47475 standard; protein; 400 AA.

AC ABR47475;
XX
DT 12-JUN-2003 (first entry)
XX
DE Breast cancer associated protein sequence SEQ ID NO:184.
XX
KW Human; breast cancer; cytostatic; gene therapy.
XX
OS Homo sapiens.

XX
PN WO2003004989-A2.
XX
PD 16-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019669.
XX
PR 21-JUN-2001; 2001US-0299887P.
XX
PR 27-JUN-2001; 2001US-0301572P.
PR 18-JUL-2001; 2001US-0306501P.
PR 25-SEP-2001; 2001US-0325002P.
PR 05-MAR-2002; 2002US-0362585P.
PR 14-MAY-2002; 2002US-0380391P.
XX
PA (MILL-) MILLENIUM PHARM INC.

XX
PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
PI Bast RC, Horcobsgyl GN, Fuszta L, Meric F, Sahin A, Mills GB;
XX
DR WPI; 2003-210381/20.
DR N-PSDB; ACC50169.
XX
PT Breast cancer diagnosis or treatment by comparing the level of expression
PT of a marker in a patient sample with that in the control non-breast
PT cancer sample.
XX
PS Claim 1; SEQ ID NO 184; 128pp; English.
XX
CC The present invention describes a method for assessing whether a patient
CC is afflicted with breast cancer. The method comprises comparing the level
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
CC ABR47386 to ABR47632) in a patient sample and the normal level of
CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences from
CC the present invention have cytostatic activities and can be used in gene
CC therapy. The method is useful for diagnosing and treating breast cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 400 AA;

Query Match 100.0%; Score 2029; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLGNGRRSMKSPPLVLAALVACIIIVLGFNWYIASSRSVDLQTRIMELEGRVRRAAERG 60
Db 1 MGLGNGRRSMKSPPLVLAALVACIIIVLGFNWYIASSRSVDLQTRIMELEGRVRRAAERG 60
QY 61 AVELKKNFQGELEKQREOLDKIOSHNFOLESVNKL YODEKAVLVNNITTTGERLIRVLQ 120
Db 61 AVELKKNFQGELEKQREOLDKIOSHNFOLESVNKL YODEKAVLVNNITTTGERLIRVLQ 120
QY 121 DOLKTLQRYNGLQODVLQFQKNQTNLERKFSYDLSQCINQMKVKEQCEERIEBVTKKG 180
Db 121 DOLKTLQRYNGLQODVLQFQKNQTNLERKFSYDLSQCINQMKVKEQCEERIEBVTKKG 180
QY 181 NEAVASRDLSNNDRQQLQALSEPQPRLOAAGLPHTPEVPOQKGNVLGNSKSTQTPAPSE 240
Db 181 NEAVASRDLSNNDRQQLQALSEPQPRLOAAGLPHTPEVPOQKGNVLGNSKSTQTPAPSE 240
QY 241 VVLDKSRQVKEETNEIQVNNEEPQDRDLPOEPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
Db 241 VVLDKSRQVKEETNEIQVNNEEPQDRDLPOEPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
QY 301 VOAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGEGDDYNNDENEASE 360
Db 301 VOAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGEGDDYNNDENEASE 360
QY 361 TDKQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400
Db 361 TDKQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400

RESULT 3
ADB75332
ID ADB75332 standard; protein; 400 AA.
XX
AC ADB75332;
XX
DT 04-DEC-2003 (first entry)
XX
DE Prostate cancer marker protein.
XX

KW Prostate; cancer; cytostatic; gene therapy; marker.

OS Homo sapiens.

XX WO2003009814-A2.

XX WO2003009814-A2.

XX PD 06-FEB-2003.

XX 25-JUL-2002; 2002WO-US023913.

XX 25-JUL-2001; 2001US-0307982P.

XX 22-AUG-2001; 2001US-0314356P.

XX 25-SEP-2001; 2001US-0325020P.

XX 12-DEC-2001; 2001US-0341746P.

XX 05-MAR-2002; 2002US-0362158P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;

XX Hoersh S, Kamatkar S, Wonsey AM, Glatk K, Zhao X, Anderson D;

XX WPI; 2003-248033/24.

XX New nucleic acid molecule, useful for diagnosing or treating prostate

XX cancer.

XX Disclosure; SEQ ID NO 156; 99pp; English.

XX The invention relates to newly discovered cancer markers associated with
CC the cancerous state of prostate cells. Also disclosed is a method of
CC assessing whether a patient is afflicted with prostate cancer. The method
CC of the invention involves assessing whether a patient is afflicted with
CC prostate cancer by comparing the level of expression of a marker in a
CC patient sample and the normal level of expression of the marker in a
CC control non-prostate cancer sample, where a significant increase in the
CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 400 AA;

Query Match 100.0%; Score 2029; DB 7; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.8e-140; Indels 0; Gaps 0;
Matches 400; Conservative 0; Mismatches 0;

QY 1 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRRAAERG 60
Db 1 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRRAAERG 60
QY 61 AVELKKNFQGLEKQREQLDKIQSHNFQLESVNKLYODEKAVLVNNTTGERLIRVLQ 120
Db 61 AVELKKNFQGLEKQREQLDKIQSHNFQLESVNKLYODEKAVLVNNTTGERLIRVLQ 120
QY 121 DQKTLQRYNGLQDDVLFQKQNTLNKRSYDLSQCINQMKVEKQCEERIEVTKKG 180
Db 121 DQKTLQRYNGLQDDVLFQKQNTLNKRSYDLSQCINQMKVEKQCEERIEVTKKG 180
QY 181 NEAVASRLSENNDORQQLALSEPPRLQAAGLPHTPEVPGKGNVGNKSKQTPAPSE 240
Db 181 NEAVASRLSENNDORQQLALSEPPRLQAAGLPHTPEVPGKGNVGNKSKQTPAPSE 240
QY 241 VVLDKSRQVKEETNEIQVNEEPQDRLPQBPGRQVVEDRPVCGRGFGGAGELGQTPQ 300
Db 241 VVLDKSRQVKEETNEIQVNEEPQDRLPQBPGRQVVEDRPVCGRGFGGAGELGQTPQ 300
QY 301 VQAAALSVQENPEMGPDPDQLVDPGQEEQEAAGEGRNQOKLRGDDYNNDENEASE 360
Db 301 VQAAALSVQENPEMGPDPDQLVDPGQEEQEAAGEGRNQOKLRGDDYNNDENEASE 360

QY 361 TDQQAALAGNDRNIDVFNVEDQKQKRDITINLLDQREKRNHTL 400
Db 361 TDQQAALAGNDRNIDVFNVEDQKQKRDITINLLDQREKRNHTL 400

RESULT 4

AAAY99368

ID AAY99368 standard; protein; 401 AA.

XX AAY99368;

XX AAY99368;

DT 08-AUG-2000 (first entry)

XX 08-AUG-2000 (first entry)

DE Human PRO1326 (UNQ686) amino acid sequence SEQ ID NO:100.

XX Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;

XX transmembrane; secretion; immunoadhesion; pharmaceutical; screening.

XX Homo sapiens.

XX WO200012708-A2.

XX 09-MAR-2000.

XX 01-SEP-1999; 99WO-US020111.

XX 01-SEP-1998; 98US-0098716P.

XX 01-SEP-1998; 98US-0098749P.

XX 01-SEP-1998; 98US-0098750P.

XX 02-SEP-1998; 98US-0098803P.

XX 02-SEP-1998; 98US-0098821P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

XX 02-SEP-1998; 98US-0098843P.

PR	24-SEP-1998;	98US-0101738P.	PR	18-NOV-1998;	98US-0108852P.
PR	24-SEP-1998;	98US-0101741P.	PR	18-NOV-1998;	98US-0108858P.
PR	24-SEP-1998;	98US-0101743P.	PR	18-NOV-1998;	98US-0108904P.
PR	24-SEP-1998;	98US-0101915P.	XX		
PR	24-SEP-1998;	98US-0101916P.	PA	(GETH) GENENTECH INC.	
PR	29-SEP-1998;	98US-0102240P.	XX		
PR	29-SEP-1998;	98US-0102240P.	PI	Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;	
PR	29-SEP-1998;	98US-0102307P.	XX		
PR	29-SEP-1998;	98US-0102330P.	DR	WPI; 2000-237871/20.	
PR	29-SEP-1998;	98US-0102331P.	DR	N-PSDB; AAA37050.	
PR	30-SEP-1998;	98US-0102484P.	XX		
PR	30-SEP-1998;	98US-0102487P.	PT	New mammalian DNA sequences encoding transmembrane, receptor or secreted	
PR	30-SEP-1998;	98US-0102570P.	PT	PRO polypeptides, useful for screening of potential peptide or small	
PR	30-SEP-1998;	98US-0102571P.	PT	molecule inhibitors of the relevant receptor/ligand interactions.	
PR	01-OCT-1998;	98US-0102684P.	XX		
PR	01-OCT-1998;	98US-0102687P.	PS	Claim 12; Fig 58; 773pp; English.	
PR	02-OCT-1998;	98US-0102965P.	XX		
PR	06-OCT-1998;	98US-0103258P.	CC	AAA37022 to AAA37144 encode the new isolated human transmembrane,	
PR	06-OCT-1998;	98US-0103449P.	CC	receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The	
PR	07-OCT-1998;	98US-0103314P.	CC	transmembrane and receptor PRO proteins can be used for screening of	
PR	07-OCT-1998;	98US-0103315P.	CC	potential peptide or small molecule inhibitors of the relevant	
PR	07-OCT-1998;	98US-0103328P.	CC	receptor/ligand interactions. The polypeptides and nucleotide sequences	
PR	07-OCT-1998;	98US-0103395P.	CC	encoding then have various industrial applications, including uses as	
PR	07-OCT-1998;	98US-0103396P.	CC	pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR	
PR	08-OCT-1998;	98US-0103401P.	CC	primers and hybridisation probes used in the isolation of the PRO	
PR	08-OCT-1998;	98US-0103633P.	CC	polypeptides from the present invention	
PR	08-OCT-1998;	98US-0103678P.	XX		
PR	08-OCT-1998;	98US-0103679P.	SQ	Sequence 401 AA;	
PR	08-OCT-1998;	98US-0103711P.			
PR	14-OCT-1998;	98US-0104257P.			
PR	20-OCT-1998;	98US-0104987P.			
PR	20-OCT-1998;	98US-0105000P.			
PR	20-OCT-1998;	98US-0105002P.			
PR	21-OCT-1998;	98US-0105104P.			
PR	22-OCT-1998;	98US-0105169P.			
PR	22-OCT-1998;	98US-0105266P.			
PR	26-OCT-1998;	98US-0105693P.			
PR	26-OCT-1998;	98US-0105694P.			
PR	27-OCT-1998;	98US-0105807P.			
PR	27-OCT-1998;	98US-0105881P.			
PR	27-OCT-1998;	98US-0105882P.			
PR	27-OCT-1998;	98US-0106062P.			
PR	28-OCT-1998;	98US-0106023P.			
PR	28-OCT-1998;	98US-0106029P.			
PR	28-OCT-1998;	98US-0106030P.			
PR	28-OCT-1998;	98US-0106032P.			
PR	28-OCT-1998;	98US-0106033P.			
PR	29-OCT-1998;	98US-0106178P.			
PR	29-OCT-1998;	98US-0106248P.			
PR	29-OCT-1998;	98US-0106384P.			
PR	29-OCT-1998;	98US-0108500P.			
PR	30-OCT-1998;	98US-0108464P.			
PR	03-NOV-1998;	98US-0106856P.			
PR	03-NOV-1998;	98US-0106902P.			
PR	03-NOV-1998;	98US-0106905P.			
PR	03-NOV-1998;	98US-0106919P.			
PR	03-NOV-1998;	98US-0106932P.			
PR	03-NOV-1998;	98US-0106934P.			
PR	10-NOV-1998;	98US-0107783P.			
PR	17-NOV-1998;	98US-0108775P.			
PR	17-NOV-1998;	98US-0108779P.			
PR	17-NOV-1998;	98US-0108787P.			
PR	17-NOV-1998;	98US-0108788P.			
PR	17-NOV-1998;	98US-0108801P.			
PR	17-NOV-1998;	98US-0108802P.			
PR	17-NOV-1998;	98US-0108806P.			
PR	17-NOV-1998;	98US-0108807P.			
PR	17-NOV-1998;	98US-0108867P.			
PR	17-NOV-1998;	98US-0108925P.			
PR	18-NOV-1998;	98US-0108848P.			
PR	18-NOV-1998;	98US-0108849P.			
PR	18-NOV-1998;	98US-0108850P.			
PR	18-NOV-1998;	98US-0108851P.			
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PR	24-SEP-1998;	98US-0101738P.	PR	18-NOV-1998;	98US-0108852P.
PR	24-SEP-1998;	98US-0101741P.	PR	18-NOV-1998;	98US-0108858P.
PR	24-SEP-1998;	98US-0101743P.	PR	18-NOV-1998;	98US-0108904P.
PR	24-SEP-1998;	98US-0101915P.	XX		
PR	24-SEP-1998;	98US-0101916P.	PA	(GETH) GENENTECH INC.	
PR	29-SEP-1998;	98US-0102240P.	XX		
PR	29-SEP-1998;	98US-0102240P.	PI	Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;	
PR	29-SEP-1998;	98US-0102307P.	XX		
PR	29-SEP-1998;	98US-0102330P.	DR	WPI; 2000-237871/20.	
PR	29-SEP-1998;	98US-0102331P.	DR	N-PSDB; AAA37050.	
PR	30-SEP-1998;	98US-0102484P.	XX		
PR	30-SEP-1998;	98US-0102487P.	PT	New mammalian DNA sequences encoding transmembrane, receptor or secreted	
PR	30-SEP-1998;	98US-0102570P.	PT	PRO polypeptides, useful for screening of potential peptide or small	
PR	30-SEP-1998;	98US-0102571P.	PT	molecule inhibitors of the relevant receptor/ligand interactions.	
PR	01-OCT-1998;	98US-0102684P.	XX		
PR	01-OCT-1998;	98US-0102687P.	PS	Claim 12; Fig 58; 773pp; English.	
PR	02-OCT-1998;	98US-0102965P.	XX		
PR	06-OCT-1998;	98US-0103258P.	CC	AAA37022 to AAA37144 encode the new isolated human transmembrane,	
PR	06-OCT-1998;	98US-0103449P.	CC	receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The	
PR	07-OCT-1998;	98US-0103314P.	CC	transmembrane and receptor PRO proteins can be used for screening of	
PR	07-OCT-1998;	98US-0103315P.	CC	potential peptide or small molecule inhibitors of the relevant	
PR	07-OCT-1998;	98US-0103328P.	CC	receptor/ligand interactions. The polypeptides and nucleotide sequences	
PR	07-OCT-1998;	98US-0103395P.	CC	encoding then have various industrial applications, including uses as	
PR	07-OCT-1998;	98US-0103396P.	CC	pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR	
PR	08-OCT-1998;	98US-0103401P.	CC	primers and hybridisation probes used in the isolation of the PRO	
PR	08-OCT-1998;	98US-0103633P.	CC	polypeptides from the present invention	
PR	08-OCT-1998;	98US-0103678P.	XX		
PR	08-OCT-1998;	98US-0103679P.	SQ	Sequence 401 AA;	
PR	08-OCT-1998;	98US-0103711P.			
PR	14-OCT-1998;	98US-0104257P.			
PR	20-OCT-1998;	98US-0104987P.			
PR	20-OCT-1998;	98US-0105000P.			
PR	20-OCT-1998;	98US-0105002P.			
PR	21-OCT-1998;	98US-0105104P.			
PR	22-OCT-1998;	98US-0105169P.			
PR	22-OCT-1998;	98US-0105266P.			
PR	26-OCT-1998;	98US-0105693P.			
PR	26-OCT-1998;	98US-0105694P.			
PR	27-OCT-1998;	98US-0105807P.			
PR	27-OCT-1998;	98US-0105881P.			
PR	27-OCT-1998;	98US-0105882P.			
PR	27-OCT-1998;	98US-0106062P.			
PR	28-OCT-1998;	98US-0106023P.			
PR	28-OCT-1998;	98US-0106029P.			
PR	28-OCT-1998;	98US-0106030P.			
PR	28-OCT-1998;	98US-0106032P.			
PR	28-OCT-1998;	98US-0106033P.			
PR	29-OCT-1998;	98US-0106178P.			
PR	29-OCT-1998;	98US-0106248P.			
PR	29-OCT-1998;	98US-0106384P.			
PR	29-OCT-1998;	98US-0108500P.			
PR	30-OCT-1998;	98US-0108464P.			
PR	03-NOV-1998;	98US-0106856P.			
PR	03-NOV-1998;	98US-0106902P.			
PR	03-NOV-1998;	98US-0106905P.			
PR	03-NOV-1998;	98US-0106919P.			
PR	03-NOV-1998;	98US-0106932P.			
PR	03-NOV-1998;	98US-0106934P.			
PR	10-NOV-1998;	98US-0107783P.			
PR	17-NOV-1998;	98US-0108775P.			
PR	17-NOV-1998;	98US-0108779P.			
PR	17-NOV-1998;	98US-0108787P.			
PR	17-NOV-1998;	98US-0108788P.			
PR	17-NOV-1998;	98US-0108801P.			
PR	17-NOV-1998;	98US-0108802P.			
PR	17-NOV-1998;	98US-0108806P.			
PR	17-NOV-1998;	98US-0108807P.			
PR	17-NOV-1998;	98US-0108867P.			
PR	17-NOV-1998;	98US-0108925P.			
PR	18-NOV-1998;	98US-0108848P.			
PR	18-NOV-1998;	98US-0108849P.			
PR	18-NOV-1998;	98US-0108850P.			
PR	18-NOV-1998;	98US-0108851P.			
<hr/>					
PR	24-SEP-1998;	98US-0101738P.	PR	18-NOV-1998;	98US-0108852P.
PR	24-SEP-1998;	98US-0101741P.	PR	18-NOV-1998;	98US-0108858P.
PR	24-SEP-1998;	98US-0101743P.	PR	18-NOV-1998;	98US-0108904P.
PR	24-SEP-1998;	98US-0101915P.	XX		
PR	24-SEP-1998;	98US-0101916P.	PA	(GETH) GENENTECH INC.	
PR	29-SEP-1998;	98US-0102240P.	XX		
PR	29-SEP-1998;	98US-0102240P.	PI	Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;	
PR	29-SEP-1998;	98US-0102307P.	XX		
PR	29-SEP-1998;	98US-0102330P.	DR	WPI; 2000-237871/20.	
PR	29-SEP-1998;	98US-0102331P.	DR	N-PSDB; AAA37050.	
PR	30-SEP-1998;	98US-0102484P.	XX		
PR	30-SEP-1998;	98US-0102487P.	PT	New mammalian DNA sequences encoding transmembrane, receptor or secreted	
PR	30-SEP-1998;	98US-0102570P.	PT	PRO polypeptides, useful for screening of potential peptide or small	
PR	30-SEP-1998;	98US-0102571P.	PT	molecule inhibitors of the relevant receptor/ligand interactions.	
PR	01-OCT-1998;	98US-0102684P.	XX		
PR	01-OCT-1998;	98US-0102687P.	PS	Claim 12; Fig 58; 773pp; English.	
PR	02-OCT-1998;	98US-0102965P.	XX		
PR	06-OCT-1998;	98US-0103258P.	CC	AAA37022 to AAA37144 encode the new isolated human transmembrane,	
PR	06-OCT-1998;	98US-0103449P.	CC	receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The	
PR	07-OCT-1998;	98US-0103314P.	CC	transmembrane and receptor PRO proteins can be used for screening of	
PR	07-OCT-1998;	98US-0103315P.	CC	potential peptide or small molecule inhibitors of the relevant	
PR	07-OCT-1998;	98US-0103328P.	CC	receptor/ligand interactions. The polypeptides and nucleotide sequences	
PR	07-OCT-1998;	98US-0103395P.	CC	encoding then have various industrial applications, including uses as	
PR	07-OCT-1998;	98US-0103396P.	CC	pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR	
PR	08-OCT-1998;	98US-0103401P.	CC	primers and hybridisation probes used in the isolation of the PRO	
PR	08-OCT-1998;	98US-0103633P.	CC	polypeptides from the present invention	
PR	08-OCT-1998;	98US-0103678P.	XX		
PR	08-OCT-1998;	98US-0103679P.	SQ	Sequence 401 AA;	
PR	08-OCT-1998;	98US-0103711P.			
PR	14-OCT-1998;	98US-0104257P.			
PR	20-OCT-1998;	98US-0104987P.			
PR	20-OCT-1998;	98US-0105000P.			
PR	20-OCT-1998;	98US-0105002P.			
PR	21-OCT-1998;	98US-0105104P.			
PR	22-OCT-1998;	98US-0105169P.			
PR	22-OCT-1998;	98US-0105266P.			
PR	26-OCT-1998;	98US-0105693P.			
PR	26-OCT-1998;	98US-0105694P.			
PR	27-OCT-1998;	98US-0105807P.			
PR	27-OCT-1998;	98US-0105881P.			
PR	27-OCT-1998;	98US-0105882P.			
PR	27-OCT-1998;	98US-0106062P.			
PR	28-OCT-1998;	98US-0106023P.			
PR	28-OCT-1998;	98US-0106029P.			
PR	28-OCT-1998;	98US-0106030P.			
PR	28-OCT-1998;	98US-0106032P.			
PR	28-OCT-1998;	98US-0106033P.			
PR	29-OCT-1998;	98US-0106178P.			
PR	29-OCT-1998;	98US-0106248P.			
PR	29-OCT-1998;	98US-0106384P.			
PR	29-OCT-1998;	98US-0108500P.			
PR	30-OCT-1998;	98US-0108464P.			
PR	03-NOV-1998;	98US-0106856P.			
PR	03-NOV-1998;	98US-0106902P.			
PR	03-NOV-1998;	98US-0106905P.</			

XX Unidentified.
 XX WO200078961-A1.
 XX PD 28-DEC-2000.
 XX PF 18-FEB-2000; 2000WO-US004342.
 XX PR 23-JUN-1999; 99US-0141037P.
 XX PR 20-JUL-1999; 99US-0144758P.
 XX PR 26-JUL-1999; 99US-0145698P.
 XX PR 01-SEP-1999; 99WO-US020111.
 XX PR 29-OCT-1999; 99US-0162506P.
 XX PR 30-NOV-1999; 99WO-US028313.
 XX PR 02-DEC-1999; 99WO-US028551.
 XX PR 16-DEC-1999; 99WO-US030095.
 XX PR 05-JAN-2000; 2000WO-US000219.
 XX PR 06-JAN-2000; 2000WO-US000376.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski RJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX WPI; 2001-071395/08.
 XX Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy.
 XX Claim 1; Fig 58; 787pp; English.
 XX The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of anti-
 CC sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy
 XX Sequence 401 AA;
 SQ
 Query Match 100.0%; Score 2029; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 5.8e-140; Indels 0; Gaps 0;
 Matches 400; Conservative 0; Mismatches 0;
 QY 1 MGLNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSYVDLQTRIMELEGRVRRAAERG 60
 Db 2 MGLNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSYVDLQTRIMELEGRVRRAAERG 61
 QY 61 AVELKKNFQGLEKQREQLDKIQSHNFKLSVKNLQDEKAVLVNNTTGERLIRVLQ 120
 Db 62 AVELKKNFQGLEKQREQLDKIQSHNFKLSVKNLQDEKAVLVNNTTGERLIRVLQ 121
 QY 121 DQKTLQRYNGLQDVLQFQKQNTNLERKFSYDLSQCNQMKVEKCEERIIEVTKKG 180
 Db 122 DQKTLQRYNGLQDVLQFQKQNTNLERKFSYDLSQCNQMKVEKCEERIIEVTKKG 181
 QY 181 NEAVASRLSENDRQQLQALSEFPRLQAAGLPHTPEVPGKGNVLGNSKSKTAPASSE 240
 Db 182 NEAVASRLSENDRQQLQALSEFPRLQAAGLPHTPEVPGKGNVLGNSKSKTAPASSE 241
 QY 241 VVLDKQVKEETNEIQVNEEPORDRLPQPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
 Db 242 VVLDKQVKEETNEIQVNEEPORDRLPQPGREQVVEDRPVGGRGFGGAGELGQTPQ 301
 QY 301 VQAAALSQENPEMGPGRDQLVDPGQEEQEAAGEGRNQKLRGEDDYNDNEAESE 360
 Db 302 VQAAALSQENPEMGPGRDQLVDPGQEEQEAAGEGRNQKLRGEDDYNDNEAESE 361

QY 361 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 400
 Db 362 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 401
 RESULT 6
 AAU12414
 ID AAU12414 standard; protein; 401 AA.
 XX AC AAU12414;
 XX DT 24-OCT-2001 (first entry)
 XX DE Human PRO1326 polypeptide sequence.
 XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIA; gene therapy.
 XX OS Homo sapiens.
 XX WO200140466-A2.
 XX PD 07-JUN-2001.
 XX PF 01-DEC-2000; 2000WO-US032678.
 XX PR 01-DEC-1999; 99WO-US028301.
 XX PR 01-DEC-1999; 99WO-US028634.
 XX PR 02-DEC-1999; 99WO-US028551.
 XX PR 02-DEC-1999; 99WO-US028564.
 XX PR 02-DEC-1999; 99WO-US028565.
 XX PR 09-DEC-1999; 99US-0170262P.
 XX PR 16-DEC-1999; 99WO-US030095.
 XX PR 20-DEC-1999; 99WO-US030911.
 XX PR 20-DEC-1999; 99WO-US030999.
 XX PR 30-DEC-1999; 99WO-US031243.
 XX PR 30-DEC-1999; 99WO-US031274.
 XX PR 05-JAN-2000; 2000WO-US000219.
 XX PR 06-JAN-2000; 2000WO-US000277.
 XX PR 11-FEB-2000; 2000WO-US003565.
 XX PR 18-FEB-2000; 2000WO-US004341.
 XX PR 18-FEB-2000; 2000WO-US004342.
 XX PR 22-FEB-2000; 2000WO-US004414.
 XX PR 24-FEB-2000; 2000WO-US004914.
 XX PR 24-FEB-2000; 2000WO-US005004.
 XX PR 01-MAR-2000; 2000WO-US005601.
 XX PR 02-MAR-2000; 2000WO-US005841.
 XX PR 03-MAR-2000; 2000US-0187202P.
 XX PR 10-MAR-2000; 2000WO-US006319.
 XX PR 15-MAR-2000; 2000WO-US006884.
 XX PR 20-MAR-2000; 2000WO-US007377.
 XX PR 21-MAR-2000; 2000WO-US007532.
 XX PR 30-MAR-2000; 2000WO-US008439.
 XX PR 17-MAY-2000; 2000WO-US013705.
 XX PR 22-MAY-2000; 2000WO-US014042.
 XX PR 30-MAY-2000; 2000WO-US014941.
 XX PR 02-JUN-2000; 2000WO-US015264.
 XX PR 05-JUN-2000; 2000US-0209832P.
 XX PR 28-JUL-2000; 2000WO-US020710.
 XX PR 11-AUG-2000; 2000WO-US022031.
 XX PR 23-AUG-2000; 2000WO-US023522.
 XX PR 24-AUG-2000; 2000WO-US023328.
 XX PR 08-NOV-2000; 2000WO-US030952.
 XX PR 10-NOV-2000; 2000WO-US030873.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, Deforge L, Desnovers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-408281/43.
 DR N-PSDB; AAS21486.
 XX
 PT Isolated , secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX
 PS Claim 12; Fig 486; 813pp; English.
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX
 SQ Sequence 401 AA;
 Query Match 100.0%; Score 2029; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 5.8e-140;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 60
 DB 2 MGLNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 61
 QY 61 AVELKKNFQGELEKQREQLDKIOSSHNFOLESVNKLQDEKAVLVNNTTGERLIRVLQ 120
 DB 62 AVELKKNFQGELEKQREQLDKIOSSHNFOLESVNKLQDEKAVLVNNTTGERLIRVLQ 121
 QY 121 DQKTLQRYNRYGLQDVLQFQKNQTNLERKFSYDLSCINQMKEVKEQCEERIEEVTKKG 180
 DB 122 DQKTLQRYNRYGLQDVLQFQKNQTNLERKFSYDLSCINQMKEVKEQCEERIEEVTKKG 181
 QY 181 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTPEVPGKGNVGNLSKSTQTPAPSE 240
 DB 182 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTPEVPGKGNVGNLSKSTQTPAPSE 241
 QY 241 VVLDKRVQVEKETNEIOVNVNEEPQDRLLPQPGREQVVEDRPGRGFGGAGELGQTPQ 300
 DB 242 VVLDKRVQVEKETNEIOVNVNEEPQDRLLPQPGREQVVEDRPGRGFGGAGELGQTPQ 301
 QY 301 VQAAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGEDDYNNDENEAESE 360
 DB 302 VQAAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGEDDYNNDENEAESE 361
 QY 361 TDKQAALAGNDRNIDVFNVEDQKRTDINLLDQREKRNHTL 400
 DB 362 TDKQAALAGNDRNIDVFNVEDQKRTDINLLDQREKRNHTL 401
 RESULT 7
 AAB49770
 ID AAB49770 standard; protein; 401 AA.
 XX
 AC AAB49770;
 XX

DT 20-APR-2001 (first entry)
 XX
 DE Amyloid-beta protein agglutination regulating factor SEQ ID 8.
 XX
 KW Human; amyloid-beta protein; agglutination regulatory factor;
 KW Alzheimer's disease.
 OS Homo sapiens.
 XX
 FN WO200104299-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 06-JUL-2000; 2000WO-JP004515.
 XX
 PR 08-JUL-1999; 99JP-00194179.
 PR 18-OCT-1999; 99US-0159586P.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Yamazaki M, Satoh S;
 PI Arakawa H, Morita M;
 XX
 DR WPI; 2001-138347/14.
 DR N-PSDB; AAF29360.
 XX
 PT Polynucleotide encoding Amyloid-beta protein agglutination-controlling
 PT factor, useful for inhibiting or promoting agglutination or sedimentation
 PT of amyloid-beta protein and in diagnosis and screening drugs for
 PT Alzheimer's disease.
 XX
 PS Claim 1; Page 56-58; 72pp; Japanese.
 XX
 CC This invention relates to polynucleotides AAF29357 - AAF29361 which
 CC encode proteins AAB49767 - AAB49771. The proteins inhibit or promote the
 CC agglutination of amyloid beta protein. The protein and polynucleotide
 CC sequences are useful in the diagnosis of Alzheimer's disease. They are
 CC also useful for screening drugs which are useful for treating Alzheimer's
 CC disease
 XX
 SQ Sequence 401 AA;
 Query Match 100.0%; Score 2029; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 5.8e-140;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 60
 DB 2 MGLNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 61
 QY 61 AVELKKNFQGELEKQREQLDKIOSSHNFOLESVNKLQDEKAVLVNNTTGERLIRVLQ 120
 DB 62 AVELKKNFQGELEKQREQLDKIOSSHNFOLESVNKLQDEKAVLVNNTTGERLIRVLQ 121
 QY 121 DQKTLQRYNRYGLQDVLQFQKNQTNLERKFSYDLSCINQMKEVKEQCEERIEEVTKKG 180
 DB 122 DQKTLQRYNRYGLQDVLQFQKNQTNLERKFSYDLSCINQMKEVKEQCEERIEEVTKKG 181
 QY 181 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTPEVPGKGNVGNLSKSTQTPAPSE 240
 DB 182 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTPEVPGKGNVGNLSKSTQTPAPSE 241
 QY 241 VVLDKRVQVEKETNEIOVNVNEEPQDRLLPQPGREQVVEDRPGRGFGGAGELGQTPQ 300
 DB 242 VVLDKRVQVEKETNEIOVNVNEEPQDRLLPQPGREQVVEDRPGRGFGGAGELGQTPQ 301
 QY 301 VQAAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGEDDYNNDENEAESE 360
 DB 302 VQAAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGEDDYNNDENEAESE 361
 QY 361 TDKQAALAGNDRNIDVFNVEDQKRTDINLLDQREKRNHTL 400
 DB 362 TDKQAALAGNDRNIDVFNVEDQKRTDINLLDQREKRNHTL 401

Db 2 MGLNGRRSMKSPPLVLAALVACIIVLGFNTWIASRRSVDLQTRIMELEGRVRAAABRG 61
QY 61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNKLYQDEKAVLVNNITTTGERLIRVLQ 120
Db 62 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNKLYQDEKAVLVNNITTTGERLIRVLQ 121
QY 121 DQKTLQRYNRYGRLOQDVLQFQKQNTNLRKFSYDLSCINOMKEVKECEERIEBVTYKG 180
Db 122 DQKTLQRYNRYGRLOQDVLQFQKQNTNLRKFSYDLSCINOMKEVKECEERIEBVTYKG 181
QY 181 NEAVASRDLSNNDRQOLQALSEPQRLQAGLPHTVPOGKGNVGNLSKSTQTPAPSE 240
Db 182 NEAVASRDLSNNDRQOLQALSEPQRLQAGLPHTVPOGKGNVGNLSKSTQTPAPSE 241
QY 241 VVLDKQKQVEKEETNEIQVNVNEEPQDRLPQEPQREQVVEPRVPGRGFGGAGELGQTPQ 300
Db 242 VVLDKQKQVEKEETNEIQVNVNEEPQDRLPQEPQREQVVEPRVPGRGFGGAGELGQTPQ 301
QY 301 VQAALSVSQENPEMEGPERDQVLPDQGEESQEAAGEGRNQOKLGEDDYNDNEAESE 360
Db 302 VQAALSVSQENPEMEGPERDQVLPDQGEESQEAAGEGRNQOKLGEDDYNDNEAESE 361
QY 361 TDQKQALAGNDRNIDVFNVEDQKRDITNLLDQREKRNHTL 400
Db 362 TDQKQALAGNDRNIDVFNVEDQKRDITNLLDQREKRNHTL 401

RESULT 9
AAB88480
ID AAB88480 standard; protein; 401 AA.
XX
AC AAB88480;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human membrane or secretory protein clone PSEC0242.
XX
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes.
XX
OS Homo sapiens.
XX
FN EP1067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-00114090.
XX
PR 08-JUL-1999; 99JP-00194179.
PR 11-JAN-2000; 2000JP-00118775.
PR 02-MAY-2000; 2000JP-00183766.
XX
PA (HELI-) HELIX RES INST.
XX
FI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX WPI; 2001-093989/11.
DR N-PSDB; AAF93907.
XX
PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
XX gene therapy or as candidate target molecules in drug development.
PS Claim 1; SEQ ID NO 328; 609pp + Sequence Listing; English.
XX
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by AAB88317
CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
CC invention. The invention also includes methods for the production of
CC antibodies directed against the proteins, and cDNA sequences, which can
CC be used in vaccines. The polynucleotide sequences can be used in gene
CC therapy. The polynucleotide sequences and the proteins they encode may be
CC used in the prevention, treatment and diagnosis of diseases associated

AA893295
ID AAB93295 standard; protein; 401 AA.
XX
AC AAB93295;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:12357.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
FN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
FI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
FI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 12357; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any special methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 401 AA;
XX
Query Match 100.0%; Score 2029; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNTWIASRRSVDLQTRIMELEGRVRAAABRG 60
|||||

CC with inappropriate secretory protein/membrane protein expression. The
CC nucleic acids and complementary sequences may also be used as DNA probes
CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples.
CC They may also be used to study the expression and function of secretory
CC proteins/membrane polypeptides and their role in metabolism. The
CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and
CC antagonists) of expression and activity. The antibodies and antagonists
CC may also be used as therapeutic agents to down regulate expression and
CC activity. The antibodies may also be used as diagnostic agents for
CC detecting the presence of the polypeptides in samples (e.g. by enzyme
CC linked immunosorbent assay (ELISA). Examples of diseases which may be
CC treated include rheumatoid arthritis and diabetes

XX Sequence 401 AA;

SQ Query Match 100.0%; Score 2029; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAARG 60
Db 2 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAARG 61
QY 61 AVELKKNFQGELEKQREQLDKIQSHNFOLESVNKLQYDEKAVLVNNTTGERLIRVLQ 120
Db 62 AVELKKNFQGELEKQREQLDKIQSHNFOLESVNKLQYDEKAVLVNNTTGERLIRVLQ 121
QY 121 DQKTLQRYNGLQDDVLQFQKNQTNLTKFSYDLSQCINQMKVKEQCEERIEVTKKG 180
Db 122 DQKTLQRYNGLQDDVLQFQKNQTNLTKFSYDLSQCINQMKVKEQCEERIEVTKKG 181
QY 181 NEAVASRLSENNDORQQLSEPPRLQAAGLPHTVEVPQKGNVLGNSKSTPAPSE 240
Db 182 NEAVASRLSENNDORQQLSEPPRLQAAGLPHTVEVPQKGNVLGNSKSTPAPSE 241
QY 241 VVLDKROVEKETNEIQVNEEPQDRDLPOPGREQVVEDRPVGRGFGGAGELGQTPQ 300
Db 242 VVLDKROVEKETNEIQVNEEPQDRDLPOPGREQVVEDRPVGRGFGGAGELGQTPQ 301
QY 301 VQAAALSVQENPEMGPEDQLVIFDQGEAEQAAAGEGRNQKLRGDDYNNDEAESE 360
Db 302 VQAAALSVQENPEMGPEDQLVIFDQGEAEQAAAGEGRNQKLRGDDYNNDEAESE 361
QY 361 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 400
Db 362 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 401

RESULT 10
ABP65020
ID ABP65020 standard; protein; 401 AA.

XX AC ABP65020;

DT 25-FEB-2003 (first entry)

XX DE Human protein SEQ ID 680.

XX KW Human; expressed sequence tag; EST; haematopoietic disorder;
KW central nervous system disease; viral infection;
KW peripheral nervous system disease; non-healing wound; infectious disease;
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;
KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;
KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;
KW immunostimulant; cerebroprotective.

XX OS Homo sapiens.

XX FN WO200259260-A2.

XX

PD 01-AUG-2002.
XX
XX 16-NOV-2001; 2001WO-US042950.
XX
PR 17-NOV-2000; 2000US-00714936.
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
PI Ren F, Xue AU, Yang Y, Wehrman T, Drmanac RT;
XX WPI; 2002-590824/63.
DR N-PSDB; ABQ99606.
XX
PT New isolated polynucleotide, useful in research, diagnostic or
PT therapeutic methods, e.g. preventing or treating disorders involving
PT aberrant protein expression or biological activity.
XX
PS Claim 20; SEQ ID NO 680; 394pp; English.
XX
CC The present invention relates to novel human coding sequences (ABQ9268-
CC ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in
CC therapeutic, diagnostic and research methods. The polynucleotides may be
CC used in the field of molecular biology as hybridisation probes, primers
CC for PCR, for chromosome and gene mapping, for the recombinant production
CC of protein, or in generation of anti-sense DNA or RNA. The
CC polynucleotides are useful in diagnostics as expressed sequence tags
CC (ESTs) for identifying expressed genes or for physical mapping of the
CC human genome. The proteins may be used as molecular weight markers, or as
CC nutritional sources or supplements. The proteins may be used to maintain
CC and expand cell population in a totipotent or pluripotential state
CC useful for re-engineering damaged or diseased tissues, transplantation,
CC manufacture of bio-pharmaceuticals or the development of bio-sensors. The
CC polynucleotides and proteins are useful for preventing, treating or
CC ameliorating disorders involving aberrant protein expression or
CC biological activity, e.g. haematopoietic disorders, central/peripheral
CC nervous system diseases, mechanical and traumatic disorders, non-healing
CC wounds, immune deficiencies and disorders, infectious diseases caused by
CC viral, bacterial or fungal infection, autoimmune disorders, allergic
CC reactions and conditions, coagulation disorders, or cancer. The
CC polynucleotide sequences of the invention were assembled from ESTs
CC isolated mainly by sequencing by hybridisation, and in some cases,
CC sequences obtained from one or more public databases. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 401 AA;

Query Match 100.0%; Score 2029; DB 5; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAARG 60

Db 2 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAARG 61

QY 61 AVELKKNFQGELEKQREQLDKIQSHNFOLESVNKLQYDEKAVLVNNTTGERLIRVLQ 120

Db 62 AVELKKNFQGELEKQREQLDKIQSHNFOLESVNKLQYDEKAVLVNNTTGERLIRVLQ 121

QY 121 DQKTLQRYNGLQDDVLQFQKNQTNLTKFSYDLSQCINQMKVKEQCEERIEVTKKG 180

Db 122 DQKTLQRYNGLQDDVLQFQKNQTNLTKFSYDLSQCINQMKVKEQCEERIEVTKKG 181

QY 181 NEAVASRLSENNDORQQLSEPPRLQAAGLPHTVEVPQKGNVLGNSKSTPAPSE 240

Db 182 NEAVASRLSENNDORQQLSEPPRLQAAGLPHTVEVPQKGNVLGNSKSTPAPSE 241

QY 241 VVLDKROVEKETNEIQVNEEPQDRDLPOPGREQVVEDRPVGRGFGGAGELGQTPQ 300

Db 242 VVLDKROVEKETNEIQVNEEPQDRDLPOPGREQVVEDRPVGRGFGGAGELGQTPQ 301

QY 301 VOALSVQENPEMGPEDQVLPDQGEAEAGBNQOKLRGDDYNNDENEARSE 360
 Db |||||
 QY 361 TDQQAALAGNDRNIDFVNEQDKRTINLLDQREKRNHTL 400
 Db |||||
 RESULT 11
 ID ABO17858
 XX ABO17858 standard; protein; 401 AA.
 AC ABO17858;
 XX
 DT 26-AUG-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO1326.
 XX
 KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
 KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
 KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
 KW TNF-alpha release; cell proliferation; cell differentiation;
 KW gene expression modulator; proteoglycan release; cytokine release;
 KW tumour; inflammatory disease; organ failure; atherosclerosis;
 KW cardiac injury; infertility; birth defect; premature aging; AIDS;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
 KW bioreactor; tissue typing.
 XX
 OS Homo sapiens.
 XX
 PN US2003032156-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 06-MAY-2002; 2002US-00140474.
 XX
 PR 31-MAR-1997; 97WO-US005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 20-NOV-1998; 98WO-US022992.
 PR 01-DEC-1998; 98WO-US024855.
 PR 05-JAN-1999; 98WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 20-APR-1999; 99WO-US008615.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 22-DEC-1999; 99WO-US030720.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US020231.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-341980/32.
 DR N-PSDB; ACD24095.

XX New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 12; Fig 486; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 401 AA;

Query Match 100.0%; Score 2029; DB 6; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLNGRSMKSPPLVLAALVACIIIVGNFYWIASRSVVDLQTRIMELEGRVRRAAERG 60
DB 2 MGLNGRSMKSPPLVLAALVACIIIVGNFYWIASRSVVDLQTRIMELEGRVRRAAERG 61

QY 61 AVELKKNFQGELEKQREQLDKIQSHNFQLESVNKLYQDEKAVLVNNTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREQLDKIQSHNFQLESVNKLYQDEKAVLVNNTTGERLIRVLQ 121

QY 121 DQKLTQRYNGLQDVLFQKNQNLERKFSYDLSQCINQMKVEKQCEERIEEVTYKG 180
DB 122 DQKLTQRYNGLQDVLFQKNQNLERKFSYDLSQCINQMKVEKQCEERIEEVTYKG 181

QY 181 NEAVASRDLSENNDORQQLQALSEPQPLQAGLPHTPEVQKGNVLGNSKSTPAPSE 240
DB 182 NEAVASRDLSENNDORQQLQALSEPQPLQAGLPHTPEVQKGNVLGNSKSTPAPSE 241

QY 241 VVLDKRVQKEETNEIQVNEEPQDRLLPQPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
DB 242 VVLDKRVQKEETNEIQVNEEPQDRLLPQPGREQVVEDRPVGGRGFGGAGELGQTPQ 301

QY 301 VQALSVSQENPEMGPPDRQLVIPDGEHEEQAAGEGNQKLRGDDYNNDENEARSE 360
DB 302 VQALSVSQENPEMGPPDRQLVIPDGEHEEQAAGEGNQKLRGDDYNNDENEARSE 361

QY 361 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 400
DB 362 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 401

RESULT 12
ABU81112
ID ABU81112 standard; protein; 401 AA.
XX
AC ABU81112;
XX
DT 23-JUN-2003 (first entry)

XX Human PRO polypeptide #243.
DE
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
KW hearing loss; coagulation disorder; stroke; heart attack; cardiant;
KW antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic;
KW antirheumatic; auditory; cerebroprotective; angiogenic.
XX
OS Homo sapiens.
XX
XX US2003004311-A1.
XX
PD 02-JAN-2003.
XX
XX 19-DEC-2001; 2001US-00028072.
XX
PR 18-JUN-1997; 97US-0049911P.
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059122P.
PR 18-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059352P.
PR 19-SEP-1997; 97US-0059588P.
PR 24-SEP-1997; 97US-0059836P.
PR 17-OCT-1997; 97US-0062250P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 17-OCT-1997; 97US-0063755P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063082P.
PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063561P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063733P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 11-DEC-1997; 97US-0069212P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 16-DEC-1997; 97US-0069694P.
PR 23-JAN-1998; 98US-0072320P.
PR 04-FEB-1998; 98US-0073612P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 12-MAR-1998; 98US-0077791P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079294P.
PR 27-MAR-1998; 98US-0079663P.
PR 31-MAR-1998; 98US-0079728P.
PR 12-JUN-1998; 98US-0080165P.
PR 14-JUL-1998; 98WO-US012456.
PR 28-AUG-1998; 98WO-US014552.
PR 10-SEP-1998; 98WO-US017888.
PR 98WO-US018824.

PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
XX
FA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-352836/33.
XX N-PSDB; ACA67236.
XX
PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT heart attack.
XX
PS Claim 12; Fig 486; 643pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. ABU80870-ABU81144 represent the human PRO

CC polypeptides of the invention. Note: The sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipadIDentry.html
XX
SQ Sequence 401 AA;
Query Match 100.0%; Score 2029; DB 6; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLNGRRSMKSPPLVLAALVACIIIVLGFNFWIASSRVDLQTRIMELEGRRVRAAARG 60
DB 2 MGLNGRRSMKSPPLVLAALVACIIIVLGFNFWIASSRVDLQTRIMELEGRRVRAAARG 61
QY 61 AVELKQNEFQGELEKQREQLDKIOSSHNFQLESYNKLYQDEKAVLVNNTTGERLIRVLQ 120
DB 62 AVELKQNEFQGELEKQREQLDKIOSSHNFQLESYNKLYQDEKAVLVNNTTGERLIRVLQ 121
QY 121 DQLKTLQRYGRLOQDVLFQKQNTNLERKFSYDLSCINQMKVEKQCEERIEBVTYKG 180
DB 122 DQLKTLQRYGRLOQDVLFQKQNTNLERKFSYDLSCINQMKVEKQCEERIEBVTYKG 181
QY 181 NEAVASRDLSNNDRQQLQALSPQRLQAAGLPHTPEVPGQKGNVLGNSKSTPAPSE 240
DB 182 NEAVASRDLSNNDRQQLQALSPQRLQAAGLPHTPEVPGQKGNVLGNSKSTPAPSE 241
QY 241 VVLDKQKQVEKEETNEIQVNVNEEPQRDLPOEPGREQVVEDRPGRGFGGAGELGQTPQ 300
DB 242 VVLDKQKQVEKEETNEIQVNVNEEPQRDLPOEPGREQVVEDRPGRGFGGAGELGQTPQ 301
QY 301 VQAALSVSQENPENMEGPERDQLVIPDQGEERQEAAGRNQOKLGEDDYNDENEAESE 360
DB 302 VQAALSVSQENPENMEGPERDQLVIPDQGEERQEAAGRNQOKLGEDDYNDENEAESE 361
QY 361 TDQAALAGNDRNDVFNVEDQKEDTINLLDQREKRNHTL 400
DB 362 TDQAALAGNDRNDVFNVEDQKEDTINLLDQREKRNHTL 401
RESULT 13
ABU66812
ID ABU66812 standard; protein; 401 AA.
XX
AC ABU66812;
XX
XX 23-MAY-2003 (first entry)
XX
XX Human PRO polypeptide #243.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.
XX
OS Homo sapiens.
XX
FN US2003036180-A1.
XX
XX 20-FEB-2003.
XX
XX 09-MAY-2002; 2002US-00143114.
XX
XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 16-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.

PR	29-OCT-1998;	98WO-US022992.	PR	01-JUN-2001;	2001WO-US017800.
PR	20-NOV-1998;	98WO-US024855.	PR	05-JUN-2001;	2001US-00874503.
PR	01-DEC-1998;	98WO-US025108.	PR	14-JUN-2001;	2001US-00882636.
PR	05-JAN-1999;	99WO-US000106.	PR	19-JUN-2001;	2001US-00886342.
PR	08-MAR-1999;	99WO-US005028.	PR	20-JUN-2001;	2001WO-US019692.
PR	10-MAR-1999;	99WO-US005190.	PR	21-JUN-2001;	2001US-00887879.
PR	20-APR-1999;	99WO-US008615.	PR	22-JUN-2001;	2001WO-US020116.
PR	14-MAY-1999;	99WO-US010733.	PR	29-JUN-2001;	2001WO-US021066.
PR	02-JUN-1999;	99WO-US012252.	PR	09-JUL-2001;	2001WO-US021735.
PR	01-SEP-1999;	99WO-US020111.	PR	18-JUL-2001;	2001US-00908827.
PR	08-SEP-1999;	99WO-US020594.	PR	06-AUG-2001;	2001US-00924419.
PR	13-SEP-1999;	99WO-US020944.	PR	09-AUG-2001;	2001US-00927796.
PR	15-SEP-1999;	99WO-US021090.	PR	16-AUG-2001;	2001US-00931836.
PR	05-OCT-1999;	99WO-US021547.	PR	19-DEC-2001;	2001US-00028072.
PR	15-SEP-1999;	99WO-US023089.	XX		
PR	29-NOV-1999;	99WO-US028214.	PA	(GETH) GENENTECH INC.	
PR	30-NOV-1999;	99WO-US028313.	XX		
PR	30-NOV-1999;	99WO-US028409.	PI	Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;	
PR	01-DEC-1999;	99WO-US028301.	PI	Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;	
PR	01-DEC-1999;	99WO-US028634.	PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;	
PR	02-DEC-1999;	99WO-US028551.	XX		
PR	02-DEC-1999;	99WO-US028551.	XX		
PR	02-DEC-1999;	99WO-US028564.	DR	WPI: 2003-332040/31.	
PR	02-DEC-1999;	99WO-US028565.	DR	N-FSDB; ACA03845.	
PR	16-DEC-1999;	99WO-US030095.	XX		
PR	20-DEC-1999;	99WO-US030911.	PT	New secreted and transmembrane PRO nucleic acids, useful for gene	
PR	20-DEC-1999;	99WO-US030999.	PT	therapy, in chromosome and gene mapping, as chromosome markers, in tissue	
PR	22-DEC-1999;	99WO-US030720.	PT	typing, and in chromosome identification.	
PR	30-DEC-1999;	99WO-US031243.	XX		
PR	30-DEC-1999;	99WO-US031274.	PS	Claim 12; Fig 486; 660pp; English.	
PR	05-JAN-2000;	2000WO-US000219.	XX		
PR	06-JAN-2000;	2000WO-US000277.	CC	The present invention relates to the isolation of novel human PRO	
PR	06-JAN-2000;	2000WO-US000376.	CC	polypeptides, and the polynucleotide sequences encoding them. The PRO	
PR	11-FEB-2000;	2000WO-US000365.	CC	polypeptides are secreted and transmembrane proteins. The PRO	
PR	18-FEB-2000;	2000WO-US004341.	CC	polypeptides are useful for detecting other PRO polypeptides, for linking	
PR	18-FEB-2000;	2000WO-US004342.	CC	polypeptides are useful for detecting other PRO polypeptides, for modulating	
PR	22-FEB-2000;	2000WO-US004414.	CC	biological activities of cells expressing PRO polypeptides, for identifying	
PR	24-FEB-2000;	2000WO-US004914.	CC	agonists or antagonists. The PRO polypeptides are useful for	
PR	01-MAR-2000;	2000WO-US005004.	CC	identifying agonists or antagonists. The PRO polypeptides are useful for	
PR	01-MAR-2000;	2000WO-US005601.	CC	stimulating the release of tumour necrosis factor (TNF)-alpha from	
PR	02-MAR-2000;	2000WO-US005746.	CC	human blood, for stimulating the proliferation or differentiation of	
PR	02-MAR-2000;	2000WO-US005841.	CC	chondrocytes, and detecting the presence of tumours. The polynucleotide	
PR	10-MAR-2000;	2000WO-US006319.	CC	sequences encoding PRO polypeptides are useful as hybridisation probes,	
PR	15-MAR-2000;	2000WO-US006884.	CC	in chromosome and gene mapping, in the generation of antisense RNA and	
PR	20-MAR-2000;	2000WO-US007377.	CC	DNA, in the preparation of PRO polypeptides, for generating transgenic	
PR	21-MAR-2000;	2000WO-US007532.	CC	animals or knockout animals, for the genetic analysis of individuals with	
PR	30-MAR-2000;	2000WO-US008439.	CC	genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the	
PR	17-MAY-2000;	2000WO-US013705.	CC	human PRO polypeptides of the invention. Note: The sequence data for this	
PR	22-MAY-2000;	2000WO-US014042.	CC	patent was obtained in electronic format directly from the USPTO web site	
PR	30-MAY-2000;	2000WO-US014941.	CC	at seqdata.uspto.gov/psipdsIDentry.html	
PR	02-JUN-2000;	2000WO-US015264.	XX		
PR	28-JUL-2000;	2000WO-US020710.	SQ	Sequence 401 AA;	
PR	11-AUG-2000;	2000WO-US022031.		Query Match 100.0%; Score 2029; DB 6; Length 401;	
PR	23-AUG-2000;	2000WO-US023522.		Best Local Similarity 100.0%; Pred. No. 5.8e-140;	
PR	24-AUG-2000;	2000WO-US023328.		Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
PR	08-NOV-2000;	2000WO-US030952.	QY	1 MGLNGRESMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRAAERG 60	
PR	10-NOV-2000;	2000WO-US030873.	Db	2 MGLNGRESMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRAAERG 61	
PR	01-DEC-2000;	2000WO-US032678.			
PR	20-DEC-2000;	2000US-00747259.			
PR	20-DEC-2000;	2000WO-US034956.			
PR	28-FEB-2001;	2001US-00796498.	QY	61 AVELKNEFOGELEKQREQLDKIQSSHNFQLESVKNLYODEKAVLVNNTTGERLIRVLQ 120	
PR	28-FEB-2001;	2001WO-US006520.	Db	62 AVELKNEFOGELEKQREQLDKIQSSHNFQLESVKNLYODEKAVLVNNTTGERLIRVLQ 121	
PR	01-MAR-2001;	2001WO-US006666.			
PR	09-MAR-2001;	2001US-00802706.	QY	121 DOLKTLQRYNGLQODVLQFQKQNTNLERKFSYDLSQCINOMKEVKEQCEERIEEVTKKG 180	
PR	14-MAR-2001;	2001US-00808689.			
PR	22-MAR-2001;	2001US-00816744.	Db	122 DOLKTLQRYNGLQODVLQFQKQNTNLERKFSYDLSQCINOMKEVKEQCEERIEEVTKKG 181	
PR	05-APR-2001;	2001US-00828366.			
PR	10-MAY-2001;	2001US-00854208.	QY	181 NEAVASRDLSNNDRQQLALSEPPRLQAAGLPHTPEVPPQSGKGNVLGNSKSTPAPSE 240	
PR	18-MAY-2001;	2001US-00860216.	Db	182 NEAVASRDLSNNDRQQLALSEPPRLQAAGLPHTPEVPPQSGKGNVLGNSKSTPAPSE 241	
PR	25-MAY-2001;	2001US-00866028.			
PR	25-MAY-2001;	2001US-00866034.	QY	241 VLDSKROVEKETWEIOVNEEPDRLPOBPGRQVVEDPVCVGRGGGNGELGOTPO 300	
PR	25-MAY-2001;	2001WO-US017092.			
PR	01-JUN-2001;	2001US-00872035.			

Db 242 VVLSKRVKEETNEIQVNEEPQDRLLPQPGREQUVEDRVPVGRGFGGAGELGQTPQ 301
QY 301 VQAALSVSQENPEMGPDRQLVDPGQEEBQEAAGGRNQKLRGDDYNNDENEASE 360
Db 302 VQAALSVSQENPEMGPDRQLVDPGQEEBQEAAGGRNQKLRGDDYNNDENEASE 361
QY 361 TDQAALAGNDRNIDVFNVEDOKRDTINLLDQREKNHTL 400
Db 362 TDQAALAGNDRNIDVFNVEDOKRDTINLLDQREKNHTL 401

RESULT 14
ABUS9893
ID ABUS9893 standard; protein; 401 AA.
XX
AC ABUS9893;
XX
XX
DT 13-MAY-2003 (first entry)
XX
DE Novel secreted and transmembrane protein PRO1326.
XX
XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
XX US2003017563-A1.
PN
XX
PD 23-JAN-2003.
XX
XX
PF 07-MAY-2002; 2002US-00140808.
XX
XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025106.
PR 05-JAN-1999; 99WO-US000108.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 30-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US00376.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH) GENENTECH INC.
PA
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WJ, Zhang Z;
XX

DR WPI; 2003-148238/14.
DR N-PSDB; ABX89383.
XX Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
PT and/or cartilage disorders, e.g. arthritis.
XX
XX
PS Claim 12; Fig 486; 659pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
XX Sequence 401 AA;
SQ
Query Match 100.0%; Score 2029; DB 6; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLGNGRSMKSPPLVLAALVACIIVLGNFYWIASRSSVDLQTRIMELEGRVRRAAERG 60
DB 2 MGLGNGRSMKSPPLVLAALVACIIVLGNFYWIASRSSVDLQTRIMELEGRVRRAAERG 61
QY 61 AVELKKNFQGELEKQREQLDKIQSHNFQLESVNKLYQDEKAVLVNNTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREQLDKIQSHNFQLESVNKLYQDEKAVLVNNTTGERLIRVLQ 121
QY 121 DQKLTQRNYGRLOQDVLFQKQNTNLERKFSYDLSQCINQMKVEKQCEERIEBVTKKG 180
DB 122 DQKLTQRNYGRLOQDVLFQKQNTNLERKFSYDLSQCINQMKVEKQCEERIEBVTKKG 181
QY 181 NEAVASRDISENDROQLOALSEPPRLQAGLPHTTEVPQCKGNVLGNSKQTPAPSE 240
DB 182 NEAVASRDISENDROQLOALSEPPRLQAGLPHTTEVPQCKGNVLGNSKQTPAPSE 241
QY 241 VVLDKROVKEKETNEIQVNEEPQDRLPQPGREQVVEDRPPVGRGFGGAGELGQTPQ 300
DB 242 VVLDKROVKEKETNEIQVNEEPQDRLPQPGREQVVEDRPPVGRGFGGAGELGQTPQ 301
QY 301 VQAALSVSQENPEMGPEDQLVLPDQBEEQEAAGEGRNQKLRGEDDYNMENEASE 360
DB 302 VQAALSVSQENPEMGPEDQLVLPDQBEEQEAAGEGRNQKLRGEDDYNMENEASE 361
QY 361 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 400
DB 362 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 401

RESULT 15
ABO25083
ID ABO25083 standard; protein; 401 AA.
XX
AC ABO25083;
XX
DT 05-SEP-2003 (first entry)
XX
XX Human secreted/transmembrane protein (PRO) #243.
XX
XX Human; PRO; secreted protein; transmembrane protein; tumour; cytostatic;
KW gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;
KW proteoglycan; cartilage; cytokine; periphera blood mononuclear cell;
KW PMW; glucose uptake; FFA; skeletal muscle cell; adipocyte cell;
KW chondrocyte cell proliferation; chondrocyte cell differentiation;
KW pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;
KW endothelial cell; A-peptide; factor VIIA.
XX
OS Homo sapiens.
XX
PN US2003036179-A1.
XX
PD 20-FEB-2003.
XX
PF 10-MAY-2002; 2002US-00142431.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 02-JUN-1999; 99WO-US010733.
PR 01-SEP-1999; 99WO-US012252.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
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PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
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PR 18-FEB-2000; 2000WO-US004341.
PR

PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
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PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
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PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
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PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
FA (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-466355/44.
DR N-PSDB; ACD42037.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
PT PRO4978, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
XX Claim 12; Fig 486; 659pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising at least 80%
CC sequence identity to a PRO (secreted and transmembrane protein) cDNA
CC comprising a nucleic acid (a) encoding a PRO polypeptide, or its
CC extracellular domain (with or without its associated signal peptide),

CC which comprises any of the 275 120-850 residue amino acid sequences,
CC given in the specification; (b) comprising any of the 275 300-3500
CC nucleotide sequences, given in the specification; or (c) comprising the
CC full-length coding sequence of the nucleotide sequences given in the
CC specification, or of the DNA deposited under any of the American Type
CC Culture Collection (ATCC) Accession Numbers listed in the specification.
CC Also included are a vector comprising the novel nucleic acid, a host cell
CC comprising the vector, producing a PRO polypeptide, the isolated PRO
CC polypeptides detailed above, a chimeric molecule comprising the PRO
CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
CC antibody, detecting a PRO polypeptide in a sample suspected of containing a
CC the PRO polypeptide, linking a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulating at least one biological activity of a cell
CC expressing a PRO polypeptide, stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, (or proteoglycans from
CC cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),
CC modulating the uptake of glucose or FFA by skeletal muscle cells or
CC adipocyte cells, stimulating the proliferation or differentiation of
CC chondrocyte cells (or proliferation of or gene expression in pericyte
CC cells), stimulating the proliferation of inner ear utricular supporting
CC cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the
CC binding of A-peptide to factor VIIA, or differentiation of adipocyte
CC cells, detecting the presence of a tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences given
CC in the specification. The polynucleotide is useful in molecular biology,
CC including uses as hybridisation probes, in chromosome and gene mapping,
CC in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide may also be used in preparing PRO polypeptides by
CC recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptide or the
CC antibody is used in preparing a medicament for treating a condition
CC responsive to the polypeptide or antibody, such as tumours, and in
CC various diagnostic assays. The present sequence represents a PRO
CC polypeptide
XX
SQ Sequence 401 AA;

Query Match 100.0%; Score 2029; DB 6; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNTWIASRSSVDLQTRIMELEGRVRAAARG 60
DB 2 MGLNGRRSMKSPPLVLAALVACIIVLGFNTWIASRSSVDLQTRIMELEGRVRAAARG 61
QY 61 AVELKKNFQGELEKQRELDKIOSSHNFQLESYNKLYODEKAVLVNNITTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQRELDKIOSSHNFQLESYNKLYODEKAVLVNNITTTGERLIRVLQ 121
QY 121 DQLKTLQRYGRLOQDVLQFQKQNTNLERKFSYDLSCINQMKVEKQCEERIEBVTKKG 180
DB 122 DQLKTLQRYGRLOQDVLQFQKQNTNLERKFSYDLSCINQMKVEKQCEERIEBVTKKG 181
QY 181 NEAVASRLSENNDQROQLQALSEPPQRLQAAGLPHTPEVPGKGNVLGNSKSTPAPSS 240
DB 182 NEAVASRLSENNDQROQLQALSEPPQRLQAAGLPHTPEVPGKGNVLGNSKSTPAPSS 241
QY 241 VVLDKQVEKEETNEIQVNVNEEPQRLPOEPGREQVVEDRPGVGGFGGAGELGQTPQ 300
DB 242 VVLDKQVEKEETNEIQVNVNEEPQRLPOEPGREQVVEDRPGVGGFGGAGELGQTPQ 301
QY 301 VQAALYSQENPENMEGPERDQLVIPDQGEFEQEAAGEGRNQKLGEDDYNNDENAESE 360
DB 302 VQAALYSQENPENMEGPERDQLVIPDQGEFEQEAAGEGRNQKLGEDDYNNDENAESE 361
QY 361 TDQQAALAGNDRNIDVFNVEDQKRDITNLLDQREKRNHTL 400
DB 362 TDQQAALAGNDRNIDVFNVEDQKRDITNLLDQREKRNHTL 401

Search completed: June 7, 2005, 14:10:15
Job time : 165 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 13:57:30 ; Search time 170 Seconds
(without alignments)
1204.892 Million cell updates/sec

Title: US-10-759-803-2
Perfect score: 2029
Sequence: 1 MGLNGRRSMKSPPLVLAAL.....DKRDTINLLDQREKRNHTL 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2029	100.0	401	1 GP73_HUMAN	Q8nbj4 homo sapien
2	1196.5	59.0	393	1 GP73_MOUSE	Q91xa2 mus musculus
3	423	20.8	411	2 Q7ZUC8	Q7zuc8 brachydanio
4	419	20.7	410	2 Q6P0H0	Q6p0h0 brachydanio
5	416.5	20.5	355	2 Q641D4	Q641d4 xenopus lae
6	351.5	17.3	433	2 Q6P4E1	Q6p4e1 homo sapien
7	348	17.2	402	2 Q6RZW6	Q6rzw6 mus musculus
8	345.5	17.0	435	2 Q6P2L7	Q6p2l7 mus musculus
9	324	16.0	380	2 Q6UY45	Q6uy45 homo sapien
10	312	15.4	319	2 Q6RZW5	Q6rzw5 mus musculus
11	255	12.6	176	2 Q8C4Z2	Q8c4z2 mus musculus
12	241	11.9	356	2 Q7T0X8	Q7t0x8 xenopus lae
13	235	11.6	177	2 Q96EM1	Q96em1 homo sapien
14	200.5	9.9	1927	2 Q25142	Q25142 halocynthia
15	185.5	9.1	1491	2 Q75UE0	Q75ue0 lampetra ja
16	185.5	9.1	1934	2 Q75UE1	Q75ue1 lampetra ja
17	185	9.1	1934	2 Q21000	Q21000 caenorhabdi
18	184.5	9.1	1302	2 Q695C7	Q695c7 homo sapien
19	181	8.9	995	2 Q7RT39	Q7rt39 plasmodium
20	180	8.9	1332	2 Q8BQ39	Q8bq39 mus musculus
21	180	8.9	1432	2 Q7Q1I2	Q7q1i2 anopheles g
22	180	8.9	1491	2 Q7S473	Q7s473 neurospora
23	178.5	8.8	1966	1 MYSB_CABEL	P02566 caenorhabdi
24	176.5	8.7	1018	2 Q7PF85	Q7pf85 anopheles g
25	176.5	8.7	1047	2 Q9C0B4	Q9c0b4 homo sapien
26	176.5	8.7	1302	2 Q7Z2L3	Q7z2l3 homo sapien
27	176	8.7	1200	2 P73340	P73340 synechocyst
28	176	8.7	3498	2 Q20497	Q20497 caenorhabdi
29	175.5	8.6	1451	2 Q812D8	Q812d8 plasmodium
30	175.5	8.6	1935	2 Q44934	Q44934 loligo peal
31	175	8.6	1941	2 Q26079	Q26079 placopecten

RESULT 1
GP73_HUMAN
ID GP73_HUMAN STANDARD; PRT; 401 AA.
AC Q8NBj4; Q6IAF4; Q9NRB9;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Golgi phosphoprotein 2 (Golgi membrane protein GP73) (UNQ686/PRO1326).
GN Name=GOLPH2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE INITIATION, GLYCOSYLATION, TISSUE
RP SPECIFICITY, AND SUBCELLULAR LOCATION.
RC TISSUE=Liver;
RX MEDLINE=20293047; PubMed=10831838; DOI=10.1016/S0378-1119(00)00136-0;
RA Kladney R.D., Bulla G.A., Guo L., Mason A.L., Tollefson A.E.,
RA Simon D.J., Koutoubi Z., Fimmel C.J.;
RT "GP73, a novel Golgi-localized protein upregulated in viral
infection.";
RL Gene 249:53-65(2000).
RN [2]
RP SEQUENCE FROM N.A.
RP PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Shiratori A., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamiyama K., Katsuma T., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotta T.,
RA Kusano J., Togawa K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togawa S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshihara Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugeno J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;

ALIGNMENTS

32	174.5	8.6	1197	1	CING_HUMAN	Q9p2m7 homo sapien
33	174	8.6	1738	2	Q76329	Q76329 dictyosteli
34	173	8.5	1992	2	Q80ZB6	Q80ze6 mus musculu
35	173	8.5	2000	2	Q6URW6	Q6urw6 mus musculu
36	172.5	8.5	1175	2	Q9TY21	Q9ty21 drosophila
37	172.5	8.5	1201	2	O18392	O18392 drosophila
38	172.5	8.5	1936	2	Q8INZ9	Q8inz9 drosophila
39	172.5	8.5	1936	2	Q8IP00	Q8ip00 drosophila
40	172.5	8.5	1936	2	Q8IP01	Q8ip01 drosophila
41	172.5	8.5	1958	2	O96062	O96062 dugesia jap
42	172.5	8.5	1962	1	MYSB_DROME	P05661 drosophila
43	172.5	8.5	1962	2	Q8IP02	Q8ip02 drosophila
44	172.5	8.5	1993	2	Q7PF91	Q7pf91 anopheles g
45	172.5	8.5	2016	2	Q7PF90	Q7pf90 anopheles g

RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Sedhagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Weiland D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry
RT vector (pDONR201).";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SUBCELLULAR LOCATION.
RX PubMed=12191016;
RA Puri S., Bachert C., Fimmel C.J., Linstedt A.D.;
RT "Cycling of early Golgi proteins via the cell surface and endosomes
RT upon luminal pH disruption.";
RL Traffic 3:641-653(2002).
RN [7]
RP TISSUE SPECIFICITY.
RX PubMed=12029628; DOI=10.1053/jhep.2002.32525;
RA Kladney R.D., Cui X., Bulla G.A., Brunt E.M., Fimmel C.J.;
RT "Expression of GP73, a resident Golgi membrane protein, in viral and
RT nonviral liver disease.";
RL Hepatology 35:1431-1440(2002).
RN [8]
RP INDUCTION BY VIRAL INFECTION.
RX PubMed=12359426; DOI=10.1006/viro.2002.1523;
RA Kladney R.D., Tollefson A.E., Wold W.S., Fimmel C.J.;
RT "Upregulation of the Golgi protein GP73 by adenovirus infection
RT requires the E1A CtBP interaction domain.";
RL Virology 301:236-246(2002).
CC -!- FUNCTION: Unknown. Cellular response protein to viral infection.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Early Golgi.
CC Cycles via the cell surface and endosomes upon luminal pH

CC disruption.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative initiation;
CC Comment=2 isoforms, 1 (shown here) and 2, are produced by
CC alternative initiation at Met-1 and Met-11;
CC TISSUE SPECIFICITY: Widely expressed. Highly expressed in colon,
CC prostate, trachea and stomach. Expressed at lower level in testis,
CC muscle, lymphoid tissues, white blood cells and spleen.
CC Predominantly expressed by cells of the epithelial lineage.
CC Expressed at low level in normal liver. Expression significantly
CC increased in virus (HBV, HCV) infected liver. Expression does not
CC increase in liver disease due to non-viral causes (alcohol-induced
CC liver disease, autoimmune hepatitis). Increased expression in
CC hepatocytes appears to be a general feature of advanced liver
CC disease. In liver tissue from patients with adult giant-cell
CC hepatitis (GCH), it is strongly expressed in hepatocyte-derived
CC syncytial giant cells. Constitutively expressed by biliary
CC epithelial cells but not by hepatocytes.
CC -!- INDUCTION: Up-regulated in response to viral infection. Induced by
CC the E1A adenoviral protein.
CC -!- PTM: Glycosylated.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-2 is the initiator.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF236056; AAF44663.1; -
DR EMBL: AK075542; BAC11685.1; -
DR EMBL: AY358593; AAC89856.1; -
DR EMBL: CR457201; CAG33482.1; -
DR EMBL: BC001740; AAH01740.1; -
DR Genbank: HGNC:15451; GOLPH2.
DR MIM: 606804; -
DR GO: GO:0005794; C:Golgi apparatus; TAS.
DR GO: GO:0005887; C:integral to plasma membrane; TAS.
KW Alternative initiation; Coiled coil; Glycoprotein; Golgi stack;
FT Signal-anchor; Transmembrane.
FT CHAIN 1 401 Golgi phosphoprotein 2, isoform 1.
FT INIT MET 11 11 For isoform 2.
FT DOMAIN 1 12 Cytoplasmic (Potential).
FT TRANSMEM 13 35 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 36 401 Luminal (Potential).
FT DOMAIN 40 205 Coiled coil (Potential).
FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 144 144 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 398 398 N-linked (GlcNAc...) (Potential).
FT CONFLICT 249 249 Q -> R (in Ref. 4).
SQ SEQUENCE 401 AA; 45333 MW; 24C1DC31B47B5B77 CRC64;
Query Match 100.0%; Score 2029; DB 1; Length 401;
Best Local Similarity 100.0%; Pred. No. 2e-88;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLNGRESMKSPPLVLAALVACIIVLGFNWYIASSRSVDLQTRIMELEGRVRAAARG 60
DB 2 MGLNGRESMKSPPLVLAALVACIIVLGFNWYIASSRSVDLQTRIMELEGRVRAAARG 61
QY 61 AVELKKNFQCELEKQREQLDKIQSHNFQLESVKNLYODEKAVLVNNTTGERLIRVLQ 120
DB 62 AVELKKNFQCELEKQREQLDKIQSHNFQLESVKNLYODEKAVLVNNTTGERLIRVLQ 121
QY 121 DQKLTQRNYGRLOQDVLFQKQNTNLERKFTSYDLSSQICINQMKVEKCEERIEEVTKKG 180
DB 122 DQKLTQRNYGRLOQDVLFQKQNTNLERKFTSYDLSSQICINQMKVEKCEERIEEVTKKG 181
QY 181 NEAVASRDLSNNDRQOQLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSKQTPAPSE 240

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Db 182 NEAVASRDSUNNDROQQLUSEPQPRLOAAGLPHTEVPQKGNVLGNKSKSQTPAPSE 241
Qy 241 VVLDKQVKEETNEIQVNEEPQDRLPQPGREQVVEDPVGGRFGGAGELGQTPQ 300
Db 242 VVLDKQVKEETNEIQVNEEPQDRLPQPGREQVVEDPVGGRFGGAGELGQTPQ 301
Qy 301 VQAAALSVSENPENMEGPERDQVLPDQGEQEAAGEGRNQKLRGEDDYNNDENEASE 360
Db 302 VQAAALSVSENPENMEGPERDQVLPDQGEQEAAGEGRNQKLRGEDDYNNDENEASE 361
Qy 361 TDQQAALAGNDRNIDVFNVEDQKRTDINLLDQREKNHTL 400
Db 362 TDQQAALAGNDRNIDVFNVEDQKRTDINLLDQREKNHTL 401

RESULT 2
ID GP73 MOUSE STANDARD; PRT; 393 AA.
AC Q91XA2;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Golgi phosphoprotein 2 (Golgi membrane protein GP73).
GN Name=Golp2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAINE/FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Jones S.J.M., Marra M.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Unknown. Cellular response protein to viral infection
(CC By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Early Golgi.
(CC Cycles via the cell surface and endosomes upon luminal pH
(CC disruption (By similarity).
CC -!- INDUCTION: Up-regulated in response to viral infection (By
(CC similarity).
CC -!- PTM: Glycosylated (By similarity).
CC -!- CAUTION: It is uncertain whether Met-1 or Met-2 is the initiator.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; BC011152; AAH11152.1; -
DR MGD; MGI:1917329; Golp2.
```

```
KW Coiled coil; Glycoprotein; Golgi stack; Signal-anchor; Transmembrane.
FT DOMAIN 1 12 Cytoplasmic (Potential).
FT TRANSMEM 13 35 Signal-anchor for type II membrane
FT 36 protein (Potential).
FT DOMAIN 36 393 Lumenal (Potential).
FT DOMAIN 40 183 Coiled coil (Potential).
FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 144 144 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 393 AA; 44310 MW; B19897C9D6D3618F CRC64;

Query Match 59.0%; Score 1196.5; DB 1; Length 393;
Best Local Similarity 65.5%; Pred. No. 4.2e-49;
Matches 262; Conservative 51; Mismatches 68; Indels 19; Gaps 10;

Qy 1 MGLNGRRSMKSPPLVLAALVACVILVGFNFWIASSRSVLDQTRIMELEGRVRRRAAERG 60
Db 2 MGLNGRRSMKSPPLVLAALVACVILVGFNFWIASSRSVLDQTRIMELEGRVRRRAAERG 61
Qy 61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVNLKYQDEKAVLVNNITGGERLIRVLQ 120
Db 62 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVNLKYQDEKAVLVNNITGGERLIRVLQ 121
Qy 121 DQKTLQRYNGLQODVLFQKQNTLNKERSYDLSCINQWKEVKEQCEERIEVTKG 180
Db 122 DQKTLQRYNGLQODVLFQKQNTLNKERSYDLSCINQWKEVKEQCEERIEVTKG 181
Qy 181 NEAVASRDSUNNDROQQLUSEPQPRLOAAGLPHTEVPQKGNVLGNKSKSQTPAPSE 240
Db 182 NEAVASRDSUNNDROQQLUSEPQPRLOAAGLPHTEVPQKGNVLGNKSKSQTPAPSE 237
Qy 241 VVLDKQVKEETNEIQVNEEPQDRLPQPGREQVVEDPVGGRFGGAGELGQTPQ 300
Db 238 -SLGKPKQVQNEETNEIQVNEEPQDRLPQPGREQVVEDPVGGRFGGAGELGQTPQ 286
Qy 301 VQAAALSVSENPENMEGPERDQVLPDQGEQEAAGEGRNQKLRGEDDYNNDENEASE 360
Db 287 LPAGI-LARPEDSQPERQLVIRD-RQEQRAAEGGGQK--NPGDEYDMDENEASE 342
Qy 361 TDQQAALAGNDRNIDVFNVEDQKRTDINLLDQREKNHTL 400
Db 343 REKQAALAGNDRNIDVFNVEDQKRTDINLLDQREKNHTL 382

RESULT 3
Q7ZUC8
ID Q7ZUC8 PRELIMINARY; PRT; 411 AA.
AC Q7ZUC8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein zgc:56525.
GN ORFNames=zgc:56525;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Jones S.J.M., Marra M.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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[illegible]


```
QY 283 PVGG-----RGFGGAGELGOTPVQAALSVSQENPEMGPEDOLV----- 323
Db 289 PTGQPLSPMPDPSHININGPGTSKQNPSSPLQRLIPGSLNDSEPRIQTDTLLKQATKDR 348
QY 324 IPDQGE-----EFQEAAGEGRNQOKLRGDDYNDME-NEAASETDKQAALAGND 371
Db 349 VSDPHKLKQSRFFDENESVPDPQHGSKLA---DYNGDDGNVGEYADKQAEALAYNE 401

RESULT 7
Q6RZW6 PRELIMINARY; PRT; 402 AA.
AC Q6RZW6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE VGF2573 isoform 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Zhou G., Liu X., Li H.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY484583; AAR26704.1; -.
SQ SEQUENCE 402 AA; 45913 MW; 906EB9162B6A7F9A CRC64;

Query Match 17.2%; Score 348; DB 2; Length 402;
Best Local Similarity 26.5%; Pred. No. 5.2e-09;
Matches 116; Conservative 76; Mismatches 148; Indels 98; Gaps 15;

QY 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNFWIASRSVDLQTRIMELEGRRVRAAARG 60
Db 2 VGFANRRAGRLPSFVLVLLVIVLAFNYWISSRHVLLQEEVAELQGVQVTEVARG 61

QY 61 AVELKKNFQGELEKQRELDKIQ-----SSHNFQESVNKLYQDEKAVLVNNTTGER 114
Db 62 RLEKNSDLLLVDTTHKKQIDQKEADYGRLSRLQAKEGLGKRCDDKVKYLNNTSYQMA 121

QY 115 LIRVLQDLKTLQRYNGRLQODVLQFQKNQTNLERKFSYDLSQINOMKEVKEQCEERIE 174
Db 122 DIHLKEQLAEFLQOEFLQEDQLQDYRKNNYLVKRLYESFQCCQQLKELRAQHEENIK 181

QY 175 EVTKKGEAVASRDLSENNDRQQLQALSEPQPRLQAAGLPHTPEVPGKGNVLGNSKST 234
Db 182 K-----LADQFLQEQKETH-----KIQSDNGKELGRNDHGA 212

QY 235 PAPSEVVLDSKRQVEKETNEIQVNEEPQDRPLQBPGRBOVVEDRPVGRGFGGAGE 294
Db 213 P-----KNIPNVPENDANK-----NEDPSSNHLPH--GKEQL---KRVGDAGMPGVEE 255

QY 295 ---LGQTPQVQAL-----SVSQENPE-----MEGP--ERDQLVIPDQGE----- 329
Db 256 NDIAKVDLPLAGSHLNQENPSTSKQNPSPLOHIIPGNLDRPRIQDTLLKQATRORA 315

QY 330 -----EEQEAAGEGRNQOKLRGDDYNDME-NEAASETDKQAALAGNDINIDV 376
Db 316 NDFPHKLKQSRFFDENESVPDPQHGSKLA---DYNGDDGNVGEYADKQAEALAYNEEDGD 372

QY 377 FNVEDQKRDITINLLDQRE 394
Db 373 GGEEDVQDD-----BERE 385

RESULT 8
Q6P2L7 PRELIMINARY; PRT; 435 AA.
AC Q6P2L7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064446; AAH64446.1; -.
SQ SEQUENCE 435 AA; 49408 MW; C62F71B6B2FA7598 CRC64;

Query Match 17.0%; Score 345.5; DB 2; Length 435;
Best Local Similarity 26.0%; Pred. No. 7.5e-09;
Matches 115; Conservative 78; Mismatches 175; Indels 75; Gaps 12;

QY 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNFWIASRSVDLQTRIMELEGRRVRAAARG 60
Db 2 VGFANRRAGRLPSFVLVLLVIVLAFNYWISSRHVLLQEEVAELQGVQVTEVARG 61

QY 61 AVELKKNFQGELEKQRELDKIQ-----SSHNFQESVNKLYQDEKAVLVNNTTGER 114
Db 62 RLEKNSDLLLVDTTHKKQIDQKEADYGRLSRLQAKEGLGKRCDDKVKYLNNTSYQMA 121

QY 115 LIRVLQDLKTLQRYNGRLQODVLQFQKNQTNLERKFSYDLSQINOMKEVKEQCEERIE 174
Db 122 DIHLKEQLAEFLQOEFLQEDQLQDYRKNNYLVKRLYESFQCCQQLKELRAQHEENIK 181

QY 175 EVTKKGEAVASRDLSENNDRQQLQALSEPQPRLQAAGLPHTPEVPGKGNVLGNSKST 234
Db 182 KLAQDFLQEQKETHKIQSDNGKE-----LGRNDHGAPKNI PNPENDANKN 227

QY 235 PAPSEVVLDSKRQVEK-----EETNEIQVNEEPQDRPL-----QEPGREQVEDR 282
Db 228 EDPSSNHLPHGKEQLKRVGDAGMPGVEENDLAKVDELPAALKKPPVLAASQESHQTI SHL 287

QY 283 PVG---GRFGGAGELGOTPVQAALSVSQENPE-----MEGP--ERDQLVIPDQGE-- 329
Db 288 PTGQPLSPMAPGSHLNQENP-----STSKQNPSPLOHIIPGNLDRPRIQDTLLKQ 343

QY 330 -----EEQEAAGEGRNQOKLRGDDYNDME-NEAASETDKQAALAGND 371
Db 344 TEDRANDPHKLKQSRFFDENESVPDPQHGSKLA---DYNGDDGNVGEYADKQAEALAYNE 400

QY 372 RNIDVFNVEDQKRDITINLLDQRE 394
Db 401 BEDGDGGEVDVQDD-----BERE 418
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RESULT 9

Q6UY45
ID Q6UY45 PRELIMINARY; PRT; 380 AA.
AC Q6UY45
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE VFG2573.
GN ORFNames=UNQ2573;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seehagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment".
RT bioinformatics assessment".
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358086; AAQ88453.1; -.
SQ SEQUENCE 380 AA; 43332 MW; B99B88414F734501 CRC64;

Query Match 16.0%; Score 324; DB 2; Length 380;

Best Local Similarity 25.1%; Pred. No. 6.7e-08;

Matches 102; Conservative 71; Mismatches 175; Indels 58; Gaps 7;

Qy 1 MGLNGRRSMKSPPLVLAALVACIIVLGFTWIASRSVDLQTRIMELEGRRVRAAERG 60
Db 2 VFGANRRAGRLPSLVLLVLLVIVLAFNYWISSRHHVLLQEEVAELQGVQVTEVARG 61
Qy 61 AVELKNEFQGELEKQREQLDKIQ-----SSHNQFLESVNLKLYODEKAVLVNNTTGER 114
Db 62 RLEKNSDLLLVVTHKKQIDQKEADYGRLSRLQAREGLKRCEDDKVKLQNNISYQMA 121
Qy 115 LIRVLQDLKTLQRYNGRLQDLVQFQKNQTNLRFKFSYDLSQICINQMKVEKQCEERIE 174
Db 122 DIHLKEQLAEFLRQEDQLQDYRKNTYLVKRLYESFQCGQOIKELRQAHEENIK 181
Qy 175 EVTKKGNFASRDLSNNDRQQLQALSEPQRLQAAGLPHTEVPQKGNVLGNSKQ 234
Db 182 K-----LADQFLEEKQETQKIQSNDGK-----LDINNQVVPKIPKVAENVADKN 228
Qy 235 PAPSEVVLDKSRQVEKE-----ETNETQVNEEPQDRLP-----QEPGRQVVEDR 282
Db 229 EEPSSNHPHGKEQIKRGCDAGMPGIEENDLAKVDLPPALRKXPPISVSQESHQAISHL 288
Qy 283 PVGG-----RFGGAGELGQTPQVQAALSVSQENPEMGPEDQLVDPDQEE 330
Db 289 PTGQPLSPNPPDSSHINNGPSTKQNPSPQLRIPGSLNDSFPRIQTDL----- 341
Qy 331 EQEAGEGRNQKLGEDYNNDENEASESTDQKAAAGNDRNIDV 376
Db 342 -----KQATKDVSPFKLKQNDERELQMDPADYKQHFNDV 379

RESULT 10

Q6RZW5
ID Q6RZW5 PRELIMINARY; PRT; 319 AA.
AC Q6RZW5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE VFG2573 isoform 2.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA Zhou G., Liu X., Li H.;

RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY484585; AAR26705.1; -.

SQ SEQUENCE 319 AA; 36067 MW; DTD9308F3A2063FC CRC64;

Query Match 15.4%; Score 312; DB 2; Length 319;

Best Local Similarity 26.9%; Pred. No. 2e-07;

Matches 97; Conservative 64; Mismatches 137; Indels 62; Gaps 12;

Qy 1 MGLNGRRSMKSPPLVLAALVACIIVLGFTWIASRSVDLQTRIMELEGRRVRAAERG 60

Db 2 VFGANRRAGRLPSLVLLVLLVIVLAFNYWISSRHHVLLQEEVAELQGVQVTEVARG 61

Qy 61 AVELKNEFQGELEKQREQLDKIQ-----SSHNQFLESVNLKLYODEKAVLVNNTTGER 114

Db 62 RLEKNSDLLLVVTHKKQIDQKEADYGRLSRLQAREGLKRCEDDKVKLQNNISYQMA 121

Qy 115 LIRVLQDLKTLQRYNGRLQDLVQFQKNQTNLRFKFSYDLSQICINQMKVEKQCEERIE 174

Db 122 DIHLKEQLAEFLRQEDQLQDYRKNTYLVKRLYESFQCGQOIKELRQAHEENIK 181

Qy 175 EVTKKGNFASRDLSNNDRQQLQALSEPQRLQAAGLPHTEVPQKGNVLGNSKQ 234

Db 182 K-----LADQFLEEKQETH-----KIQSNDGKELGRNDHGA 212

Qy 235 PAPSEVVLDKSRQVEKEETNEIQVNEEPQDRLPQEPGRQVVEDRPGVGRFGGAGE 294

Db 213 P-----KNIPNPENDANK-----NEDPSSNHLPH-----KRGQL-----KRVGDAGMPGVEE 255

Qy 295 --LGQTPQVQAALSVSQ--ENP--EMEGPERD--QVVIP-----DGOEEQEAAGEGRNQKL 344

Db 256 NDLAKVDLPAAGSHLNQNEPSTKQNPSPQLQIIPGPNSTQNSNRHVKAGHQGQSL 315

RESULT 11

Q8C422

ID Q8C422 PRELIMINARY; PRT; 176 AA.

AC Q8C422

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched

DE library, clone:A630071M09 product:hypothetical protein, full insert

DE sequence. (Fragment).

GN Name=DI30060C09Rik;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]


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Qy 276 EQVVEDRVPVGGGFGGAGE-----LGQTPVQAAALSVSQENPEMGPGRDQLV-IPDQOE 329
Db 250 EDSJQN-DVKGQDTPGALPSQSKSLKQPSLQ-PLSFTEHEVKKPLPKKKTQVIP---E 304
Qy 330 BEQEAAGEGRNQKLRGDDNMDNEAASETDKQAAALAGNDRNIDVEN 378
Db 305 VEENALQLEPHLPKQMPDRSKTMSFNLKQKDDHDDGQADAGEYKHDLN 353

RESULT 13
Q96EM1
ID Q96EM1 PRELIMINARY; PRT; 177 AA.
AC Q96EM1
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE H63 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max A.M., Wang J., Hsieh P.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012124; AAH12124.1; -.
SQ SEQUENCE 177 AA; 20934 MW; DF8452919A90949A CRC64;

Query Match 11.6%; Score 235; DB 2; Length 177;
Best Local Similarity 33.1%; Pred. No. 0.00045;
Matches 57; Conservative 37; Mismatches 70; Indels 8; Gaps 2;

Qy 1 MGLGNRRSMKSPPLVLAALVACILVLGFNFWIASSRSVDLQTRIMELEGVRRAAERG 60
Db 2 VGFGANRRAGRLPSLVLLVLLVILVAFNFWISRRVLLQEEVAAELQGVQRTVEARG 61
Qy 61 AVELKQNEFOQLEKREQLDKIQ-----SSHNFQLESVNKLYODEKAVLVNNTTGER 114
Db 62 RLEKNSDLLLVTHKKQIDQEKADYGRLLSRRLQAREGLKRCDDKVLKNNISYQMA 121
Qy 115 LIRVLQDLKTLQRYNQLQDVLQFQKQNTNLERKFSYDLS--QCINQMK 164
Db 122 DIHHLKEQLAELRQEFRLQEDQLQDYRKQNTLVKRLYESKRPKRFNQME 173

RESULT 14
Q25142
ID Q25142 PRELIMINARY; PRT; 1927 AA.

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AC Q25142;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Embryonic muscle myosin heavy chain.
GN Name=MHCemb;
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
RA Araki I., Satoh N.;
RT "Cis-regulatory elements conserved in the proximal promoter region of
RT an ascidian embryonic muscle myosin heavy chain gene.";
RL Roux's Arch. Dev. Biol. 0:0-0(1995).
DR EMBL; D45163; BAA08111.1; -.
DR PIR; A59236; A59236.
DR HSPF; P08799; IMND.
DR GO; GO:0016459; C:myosin; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR001609; Myosin_head.
DR InterPro; IPR004009; Myosin_tail.
DR Pfam; PF00612; IQ; 2.
DR Pfam; PF00663; Myosin_head; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR SMART; SM00242; MYSC; 1.
SQ SEQUENCE 1927 AA; 222461 MW; 2F6F18A2B71BC34E CRC64;

Query Match 9.9%; Score 200.5; DB 2; Length 1927;
Best Local Similarity 23.1%; Pred. No. 0.29;
Matches 96; Conservative 57; Mismatches 151; Indels 111; Gaps 13;

Qy 40 DLQTRIMELEGVRRAAARGAVELKKNFQCELE----- 74
Db 1110 ELQARIELEEELEAARAARAKVEQRADLSRELEELSERLEEAGGATAAQIENKREA 1169
Qy 75 ---KORQLDKIQSHNFQLESVNKLYODEKAVLVNNTTGERLIRVLQDLKTLQRYN 131
Db 1170 EFSKLRLEESNLAHEATVSTLRKKHADSAEMSEQIDNLRVQKQLEKESEMKMEVD 1229
Qy 132 RLQODV-----LQFQKQNTNLERKFSYDLSQCINQMKVEKQCEERIEFVTKKGN 184
Db 1230 DLAAANVESITKAKLVYKEMARNLSEQFSKTKCDNFCKEYNEL-----NAA 1276
Qy 185 ASRDLSENNDORQQLALSEPQRLQAAGLPHTVPQKGNVLGNSKTSQTPAPSEVILD 244
Db 1277 KAFASENGELSRL-----EREHLMA-----QLTRTKNSSSQQTEE 1314
Qy 245 SKRQVEKETNEIQVNVNEEPQDRLPQEPGRQVVEDRVPVGGFGGAGELGQTPQVQAA 304
Db 1315 LKRVVE-EETKAKAALAHVQASRDNDLLREQVEEEOEA-----KAEQRA 1360
Qy 305 LSVS-----QENPEMGPGRDQLVIPDQOEEOEA-----AGEGRNOOK 343
Db 1361 LSKANAESAQWRNKYETDAIQRTTELEBAKATRLQEAEEQVEATQAKCASLDKTKNR 1420
Qy 344 LRGE-DDYNDENEASETDKQAALAGNDRNID-VFNVEDOKRTINL-LDQREK 395
Db 1421 LQGELEDITD---LERSNSAAALDKQRNFDKVLAEKQKEBEIQVELSQAOK 1472

RESULT 15
Q75UE0
ID Q75UE0 PRELIMINARY; PRT; 1491 AA.
AC Q75UE0;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 14:01:01 ; Search time 41 Seconds
(without alignments)
938.700 Million cell updates/sec

Title: US-10-759-803-2
Perfect score: 2029
Sequence: 1 MGLNGRRSMKSPPLVLAAL.....DQKEDTINLLDQREKRNHTL 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	200.5	9.9	1927	2 A59236	embryonic muscle m
2	185	9.1	1974	2 T30010	hypothetical prote
3	178.5	8.8	1963	1 MKKW	myosin heavy chain
4	176	8.7	1200	2 S77524	chromosome segrega
5	176	8.7	3498	2 T22330	hypothetical prote
6	174	8.6	1738	2 T14867	interaptin - slime
7	172.5	8.5	1175	2 C35815	myosin heavy chain
8	172.5	8.5	1201	2 A35815	myosin heavy chain
9	172	8.5	1175	2 D35815	myosin heavy chain
10	172	8.5	1201	2 B35815	myosin heavy chain
11	171.5	8.5	1164	2 T24806	hypothetical prote
12	171.5	8.5	1938	1 A40987	myosin heavy chain
13	170.5	8.4	1940	2 A59287	myosin heavy chain
14	170	8.4	2385	2 A32491	myosin heavy chain
15	170	8.4	2411	2 B32491	myosin heavy chain
16	169.5	8.4	1269	2 F84730	probable myosin he
17	168.5	8.3	1938	2 A59293	skeletal myosin he
18	168	8.3	1922	2 T00637	hypothetical prote
19	167.5	8.3	1956	2 T16416	hypothetical prote
20	167.5	8.3	1957	2 A45627	myosin heavy chain
21	167	8.2	849	2 S00030	neurofilament trip
22	167	8.2	1961	1 A61231	myosin heavy chain
23	167	8.2	3187	2 JC5837	364K Golgi complex
24	166.5	8.2	1940	1 A24922	myosin heavy chain
25	166.5	8.2	1999	1 S21801	myosin heavy chain
26	166	8.2	895	2 T45738	hypothetical prote
27	166	8.2	944	2 S26710	spindle pole body
28	166	8.2	1938	1 JX0178	myosin heavy chain
29	165.5	8.2	1940	1 S04090	myosin heavy chain

30	165	8.1	876	2 A23767	myosin heavy chain
31	165	8.1	1898	1 A45973	trichohyalin - hum
32	165	8.1	1992	2 A47297	myosin heavy chain
33	164.5	8.1	1959	1 A33977	myosin heavy chain
34	164	8.1	1138	2 T24635	hypothetical prote
35	163.5	8.1	1957	2 A59294	skeletal myosin -
36	163.5	8.1	1957	2 T38077	hypothetical coile
37	163	8.0	1940	2 A29320	myosin heavy chain
38	162.5	8.0	798	2 T50479	neurofilament medi
39	161	7.9	1133	2 T22976	hypothetical prote
40	160.5	7.9	428	1 T36930	involucrin - white
41	160.5	7.9	916	2 A27864	neurofilament trip
42	160.5	7.9	2057	2 S61477	myosin II heavy ch
43	160	7.9	447	2 T46146	hypothetical prote
44	160	7.9	936	2 S39083	myosin heavy chain
45	160	7.9	980	2 E71606	hypothetical prote

ALIGNMENTS

RESULT 1

A59236
embryonic muscle myosin heavy chain - sea squirt (Halocynthia roretzi)
C:Species: Halocynthia roretzi
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59236
R:Araki, I.
submitted to GenBank, February 1999
A:Reference number: A59236
A:Accession: A59236
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1927 <ARA>
A:Cross-references: UNIPROT:Q25142; GB:D45163; NID:g1197167; PIDN:BAA08111.1; PID:g11971
A:Experimental source: clone lib lambda gtl1; dev stage tailbud embryo
C:Genetics:
A:Gene: MHCemb
C:Superfamily: myosin heavy chain; myosin motor domain homology
F:89-766/Domain: myosin motor domain homology <MHO>

Query Match		9.9%	Score 200.5; DB 2; Length 1927;
Best Local Similarity		23.1%;	Pred. No. 0.0082;
Matches		96; Conservative	57; Mismatches 151; Indels 111; Gaps 13;
Qy	40	DLQTRIMELEGRVRRRAAERGAVELKKNFQGELE-----	74
Db	1110	ELQARIEELBEELAEARAAKAEKQADLSRELEELSERLEAGGATAAIELNKRREA	1169
Qy	75	---KQREQLDKIOSSHNFQLESVNKLYQDEKAVLVNNITTTGERLIRVLQDQLKTLQRYNG	131
Db	1170	EFSKLRLEELSESLNAHEATVSTLRKKHADSSAENSEQIDNLRVKQKLEKESKEMKMEVD	1229
Qy	132	RLQODV-----LQFOKQNTNLERKFSYDLSCQINQMKVEKQCEERIEEVTKKGNRAV	184
Db	1230	DLAANVESITKALNVEKMAKNLEEQFSSEKTKCDNFCKEVNEL-----NAA	1276
Qy	185	ASRDLSENNDORQQLALSEPQLQAAGLPHTEVPQKGNVLGNSKTSQTPAPSESVLVD	244
Db	1277	KARFASENGELSRQL-----EREHLMA-----QUTRTKNSSSQQLLEE	1314
Qy	245	SKRQVEKEETNEIOVNVNEEPQDRLPQEPQREQVVEDRPVGGRGFGGAGELGQTPQVQAA	304
Db	1315	LKRVEE-EETKAKAALAHSAVQASRHDNDLLREQVEEQEA-----KAELOQA	1360
Qy	305	LSVS-----QENDEMGPERDQVLIPDQEEQEA-----AGGRNOOK	343
Db	1361	LSKANAQVAQWRNKYETDAIQRTTEELAEAKKATRLQEAEEQVEAQKACASIDKTKNR	1420
Qy	344	LRGE-DDYNNDENEASETDKQALAGNDRNID-VFNVEDQKRTINL-LDQREK	395
Db	1421	LQGELEDLTID---LERSNSAAALDKQRNFDKVLAEKQKEEIQVELEQAOK	1472

RESULT 2

T30010
hypothetical protein F58G4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30010
R:Du, Z.; Leimbach, D.
submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid F58G4.
A:Reference number: Z20720
A:Accession: T30010
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1974 <DUZ>
A:Cross-references: UNIPROT:Q21000; EMBL:U50309; PIDN:AAB37057.1; GSPDB:GN000023; CESP:F58G4
A:Experimental source: strain Bristol N2; clone F58G4
C:Genetics:
A:Gene: CESP:F58G4.1
A:Map position: 5
A:Introns: 18/3; 111/3; 164/1; 229/1; 378/1; 440/2; 525/3; 1177/2; 1633/3; 1863/3
C:Superfamily: myosin heavy chain; myosin motor domain homology
F:84-776/Domain: myosin motor domain homology <MMO>

Query Match 9.1%; Score 185; DB 2; Length 1974;
Best Local Similarity 22.3%; Pred. No. 0.054;
Matches 90; Conservative 75; Mismatches 144; Indels 94; Gaps 15;

QY	40	DLQTRIMELEGRVRRRAAARGAVELKKNEFOGELEKQREOLDKIQSSHNFOLE-----	92
DB	1120	ELLARIQLEELDAERNRSKAEKARNQMQLBELGDLRLDEAGGATQAQIQLNKKREA	1179
QY	93	SVNKLYQDEKAVLVNNTTGERL-----TRVLDQDKTLQRYNVRLOQDVLPQKNQT	145
DB	1180	ELAKLQDLDEAAINSETSMALRKXKHNDAVAELSDQDITIQMKRGKLEKNDKQREVD	1239
QY	146	NLERKFSYDLSCINOMKEVKEQCEERIEEVTCKGNEAV-----ASRDLSENNDQR	196
DB	1240	ELQQGADYEAQRQN-CERMAKQLBAQTDMFLKSDQEARLIQELTWGKNVHNENQDLN	1298
QY	197	QQLQALSBPQLQAAGLPHTEVPQGGKGNVLGNSKSTPAPSESVVLDKQVEKETNE	256
DB	1299	RQLE---DAEAQLCA-----LNRIKQQHQSLEEL---KRTLD-QETRE	1335
QY	257	IQVNEEPQRDLPLQPGREQVVEDRPV-----GGRGFGGAGE	294
DB	1336	RQSLHSQVSNYQLECEQFRESLEERQDAKTDVQRLSKANSEIQOMRAKFEPEGVSRAE	1395
QY	295	LGQTPQVQAALSVSOENPEMEGPERDQLVIPDQEEQEAAGEGRNQOKLRGE-DDYNMD	353
DB	1396	LEETR-----KLTHKVQEMQ-----EQL-----ENANQIGTLEKKNQRLAHLDAQVD	1441
QY	354	ENAEBS-ETDKQAALAGNDRNID-----VFNVEDQKRDY	386
DB	1442	ADRANSIASLSEKKQKGFVDLWRRKCEALVAEVEQSQRET	1484

RESULT 3

MKW
myosin heavy chain B [similarity] - Caenorhabditis elegans
N:Contains: myosin ATPase (EC 3.6.4.1)
C:Species: Caenorhabditis elegans
C:Date: 13-Jun-1983 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: T20770; T21629; A93958; A93287; A21074; A02992
R:Kershaw, J.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19322
A:Accession: T20770
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1963 <WIL>
A:Cross-references: UNIPROT:Q02244; EMBL:Z81499; PIDN:CAB04089.1; GSPDB:GN000019; CESP:F11C3
A:Experimental source: clone F11C3

A:Accession: T21629
A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-1963 <WIL>
A:Cross-references: EMBL:Z83107; PIDN:CAB05505.1; GSPDB:GN000019; CESP:F11C3.3
A:Experimental source: clone F32A7
R:Karn, J.; Brenner, S.; Barnett, L.
Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983
A:Title: Protein structural domains in the Caenorhabditis elegans unc-54 myosin heavy chain
A:Reference number: A93958; MUID:83273600; PMID:6576334
A:Accession: A93958
A:Molecule type: DNA
A:Residues: 1-61, 'EMSVIQ', 65-376, 'V', 378-1963 <KAR>
A:Cross-references: GB:J01050; NID:g156399; PIDN:AAA28124.1; PID:g156400
R:McLachlan, A.D.; Karn, J.
Nature 299, 226-231, 1982
A:Title: Periodic charge distributions in the myosin rod amino acid sequence match cross
A:Reference number: A93287; MUID:82272395; PMID:7202124
A:Accession: A93287
A:Molecule type: DNA
A:Residues: 847-1333, 'R', 1335-1876, 'L', 1878-1963 <MCL>
R:Wills, N.; Gesteland, R.F.; Karn, J.; Barnett, L.; Bolten, S.; Waterston, R.H.
Cell 33, 575-583, 1983
A:Title: The genes sup-7 X and sup-5 III of Caenorhabditis elegans suppress amber nonsense
A:Reference number: A21074; MUID:83232892; PMID:6571695
A:Accession: A21074
A:Molecule type: DNA
A:Residues: 1873-1963 <W13>
A:Cross-references: GB:V01494; GB:J01049; NID:g6783; PIDN:CAA24738.1; PID:g6784
C:Genetics:
A:Gene: unc-54; CESP:F11C3.3
A:Map position: 1
A:Introns: 21/3; 64/3; 111/3; 264/1; 525/3; 951/2; 1747/3; 1819/3; 1894/3
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydroxylase; methylated amino acid; muscle coiled coil
F:84-775/Domain: myosin motor domain homology <MMOT>
F:174-181/Region: nucleotide-binding motif A (P-loop)
F:662-684/Region: actin binding #status predicted
F:766-780/Region: actin binding #status predicted
F:848-1963/Domain: coiled coil #status predicted <COI>
F:848-1162/Region: S2
F:1163-1963/Region: light meromyosin
F:125/Modified site: N6,N6-trimethyllysine (Lys) #status predicted
F:180/Binding site: ATP (Lys) #status predicted
F:702,712/Active site: Cys #status predicted

Query Match 8.8%; Score 178.5; DB 1; Length 1963;
Best Local Similarity 21.8%; Pred. No. 0.12;
Matches 90; Conservative 77; Mismatches 177; Indels 69; Gaps 13;

QY	40	DLQTRIMELEGRVRRRAAARGAVELKKNEFOGELEKQREOLDKIQSSHNFOLESVNKLYQ	99
DB	1119	DGQSRISLELEENRQSRKADRAKSDLORELEELGKLDQGGATAAQVE-VNKKRE	1177
QY	100	DEKAVLVNNTTGER-----LIRVLQDKTLQRYNVRLOQDVLPQKNQ	144
DB	1178	AELAKLRDLLEANNHNLGGLRKKHTDAVELTDQLDQLNKKAKVKDKQAQRDA	1237
QY	145	TNLERKFSYDLSCINOMKEVKEQCEERIEEVTCKGNEAVASRDLSENNDQRLQALSE	204
DB	1238	EDLAAQLDQETSGKLNKKLAK-QPELQTLQSKADE-----QSRQLQDFTS	1284
QY	205	PQPLQIQAAG---LPHTEVPQGGKGNVLGNSKSTPAPSESVVLDKQVEKETNEIQVN	261
DB	1285	LKGRLLHSENGDLVRQLEDAESQVNLTRLKSQLSQLEEARRTADEEARERQITVAAQKN	1344
QY	262	EEPQRDLPLQPGREQVVEDRPV-----GGRGFGGAGELGQTP-----	299
DB	1345	YQHEARQL-QESLEEEIEGKNEILLQLSKANADIQQWKARFEGEGLLKKADELDKAKROA	1403
QY	300	----QVQAAL-SVSOENPEMEGPERDQLVIPDQEEQEAAGEGRNQOKLRGDDVNM	352
DB	1404	QKINELQALDAANSKNASLE-KTKSRVLVGDLDDAQVDVERANGVASALEKKQKGFDKII	1462

RESULT 9

D35815
myosin heavy chain 4, muscle - fruit fly (*Drosophila melanogaster*) (fragment)
C:Species: *Drosophila melanogaster*
C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C:Accession: D35815
R:Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A>Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
A:Reference number: A35815; MUID:90346288; PMID:2116987
A:Accession: D35815
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1175 <COL>
A:Cross-references: UNIPROT:Q9TY21; EMBL:X53155
A:Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
C:Genetics:
A:Gene: FlyBase:Mhc
A:Cross-references: FlyBase:FBgn0002741
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP

```
Query Match      8.5%; Score 172; DB 2; Length 1175;
Best Local Similarity 20.6%; Pred. No. 0.14;
Matches 84; Conservative 73; Mismatches 155; Indels 96; Gaps 11;

Qy  41 LQTRIMELEGRRVRAAARGAVELKKNEFGQ-----ELEKQRLDKIOSSHNFQ 90
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  265 LEQTLDELEDSLERKKVKGVDVSKRVEGDKLTQEAADVADLERKKELSGTTQKDK 324
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  91 LESVNVLYQDEKAVLVNNTTGERLIRVLQDLKTLQRYNGLQODVLQFQKN----- 143
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  325 LSSITAKLEDEQVVLKH-----QRQIKELQARIEELEVEEAERQARAKAQADLARE 380
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  144 -----QTNLERKFSYDLSQINQMKVEKQCEERIEEVTKKNEAVAS 186
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  381 LEEGLERLEEAGGATSAQIELNKKREAEISKLRDLDEEANTQHESTLANLRKKHNDAVA- 439
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  187 RDLSENNDQROQLQALSEPQRLQ-----AAGLPH-----TEVP 220
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  440 -EMAEQVDQLNKLKAKAEKNEYVQGLNDRAGVDHITNEKAAQEKIAKQLOHTLINEV- 497
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  221 QGKGNVLGNSKSTPPAPSEVVLDK---RQVEKEETN-----EIQVNVNEEPQDRRLP 270
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  498 QSKLDETNRITLNDPASKKLSIENSLLRQLEAEASQVLSKIKISLTITQLEDTKRLA 557
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  271 QEPGREQVVEDRPVGGRGFGAGELGQTPQVQAALSVSQENPEMPEGPERDQIVPDGQEE 330
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  558 DEESRER-----ATLLGKFRNLHDLNLRREQVBEAEAGKADL-----QRQ 598
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  331 EQEAAAGEGRNQKLRGDDYNNMDNEAESETDKQAALAGNDRNIDVFN 378
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  599 LSKANAQAQWRSKYSGDVARSELEAKKQLARLAEABETIESLN 646
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 10

B35815
myosin heavy chain 2, muscle - fruit fly (*Drosophila melanogaster*) (fragment)
C:Species: *Drosophila melanogaster*
C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C:Accession: B35815
R:Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A>Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
A:Reference number: A35815; MUID:90346288; PMID:2116987
A:Accession: B35815
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1201 <COL>
A:Cross-references: UNIPROT:O18392; EMBL:X53155; NID:98219; PIDN:CAA37311.1; PID:9254693
A:Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
C:Genetics:

A:Gene: FlyBase:Mhc

A:Cross-references: FlyBase:FBgn0002741

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: ATP

Query Match 8.5%; Score 172; DB 2; Length 1201;

Best Local Similarity 20.6%; Pred. No. 0.14;

Matches 84; Conservative 73; Mismatches 155; Indels 96; Gaps 11;

```
Qy  41 LQTRIMELEGRRVRAAARGAVELKKNEFGQ-----ELEKQRLDKIOSSHNFQ 90
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  265 LEQTLDELEDSLERKKVKGVDVSKRVEGDKLTQEAADVADLERKKELSGTTQKDK 324
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Qy  91 LESVNVLYQDEKAVLVNNTTGERLIRVLQDLKTLQRYNGLQODVLQFQKN----- 143
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  325 LSSITAKLEDEQVVLKH-----QRQIKELQARIEELEVEEAERQARAKAQADLARE 380
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Qy  144 -----QTNLERKFSYDLSQINQMKVEKQCEERIEEVTKKNEAVAS 186
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  381 LEEGLERLEEAGGATSAQIELNKKREAEISKLRDLDEEANTQHESTLANLRKKHNDAVA- 439
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Qy  187 RDLSENNDQROQLQALSEPQRLQ-----AAGLPH-----TEVP 220
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  440 -EMAEQVDQLNKLKAKAEKNEYVQGLNDRAGVDHITNEKAAQEKIAKQLOHTLINEV- 497
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Qy  221 QGKGNVLGNSKSTPPAPSEVVLDK---RQVEKEETN-----EIQVNVNEEPQDRRLP 270
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  498 QSKLDETNRITLNDPASKKLSIENSLLRQLEAEASQVLSKIKISLTITQLEDTKRLA 557
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Qy  271 QEPGREQVVEDRPVGGRGFGAGELGQTPQVQAALSVSQENPEMPEGPERDQIVPDGQEE 330
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  558 DEESRER-----ATLLGKFRNLHDLNLRREQVBEAEAGKADL-----QRQ 598
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Qy  331 EQEAAAGEGRNQKLRGDDYNNMDNEAESETDKQAALAGNDRNIDVFN 378
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Db  599 LSKANAQAQWRSKYSGDVARSELEAKKQLARLAEABETIESLN 646
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Db  599 LSKANAQAQWRSKYSGDVARSELEAKKQLARLAEABETIESLN 646
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 11

hypothetical protein T10G3.5 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T24806

R:Burton, J.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19937

A:Accession: T24806

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1164 <WIL>

A:Cross-references: UNIPROT:P92021; EMBL:Z81118; PIDN:CA03330.1; GSPDB:GN00023; CESP:T.1

A:Experimental source: clone T10G3

C:Genetics:

A:Gene: CESP:T10G3.5

A:Map position: 5

A:Introns: 15/3; 73/3; 387/3; 412/3; 708/3; 818/3; 894/3; 982/3; 1080/2

Query Match

Best Local Similarity 19.6%; Pred. No. 0.15; Length 1164;

Matches 87; Conservative 80; Mismatches 154; Indels 123; Gaps 16;

```
Qy  3 LGNRRRSMKPPVLAAALVACIIIVGLPNYVITASSRSVDLQTRIMELEGRRVRAAARGAV 62
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  301 IGEGETVKQ-----LQISYDAQSELKQERNVQVLEARI-----EENVF 341
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Qy  63 ELKQNE-----FQGELEKQK---EOLDKIOSSHNFQLESVNVKLYQDEKAVLVNNTTGER 114
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  342 ELSNKQNVKRLDKVQESQDALQMLSNINGSNEEQMISLNSKPERNTAERKRIEAVPEE 401
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Qy  115 LIRVLQDLKTLQRYNGLQODVLQ-----FQKQNTNLERKFSYDLSQINQMKVEKQCE 170
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  402 KTVQGERLTKLEMANLDLTNELASMGSLDKERSLLEEK-NKEISRDSSINDLKEKLA 460
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```


R:George, E.L.; Ober, M.B.; Emerson Jr., C.P.

Mol. Cell. Biol. 9, 2957-2974, 1989

A:Title: Functional domains of the Drosophila melanogaster muscle myosin heavy-chain gene

A:Reference number: A32491; MUID:89384556; PMID:2506434

A:Accession: B32491

A:Status: preliminary

A:Molecule type: DNA; mRNA

A:Residues: 1-2385 <GEO>

A:Cross-references: UNIPROT:P05661; GB:M61229; GB:M27194

A:Note: the authors translated the codon TGC for residue 329 as Ser

C:Genetics:

A:Gene: FlyBase:Mhc

A:Cross-references: FlyBase:FBgn0002741

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: ATP; nucleotide binding; P-loop

F:137-1032/Domain: myosin motor domain homology #status atypical <MMO>

F:227-234/Region: nucleotide-binding motif A (P-loop)

Query Match 8.4%; Score 170; DB 2; Length 2385;
Best Local Similarity 20.9%; Pred. No. 0.41;
Matches 86; Conservative 77; Mismatches 148; Indels 100; Gaps 14;

Qy 41 LQTRIMELEGRVRRRAAARGAVELKNEFGQ-----ELEKQREOLDKIQSSHNQ 90

Db 1449 LEQTLDELEDSLEREKVKRGDVEKSKRVGDLKLTQEAVALDLERNKKELEQTQKDK 1508

Qy 91 LESVNLKYQDEKAVLVNNTTGERLIRVLQDLKTLQRYNGRLQDVLQFQKN----- 143

Db 1509 LSSITAKLEDEQVVVLKH---QRQIKELQARIBELEVEAEQARAKAQKQADLARE 1564

Qy 144 -----QTNLERKFSYDLSCINQMKEVKQCEBIEEVTYKKGNEAVAS 186

Db 1565 LEELGERLEEAGGATSAQIELNKKREAELSCLRDLDEEANTQHESTLANLRKKHNDAVA- 1623

Qy 187 RDLSENNDQROQLALSEPQPRLOAAGLPHTVEVPGKGNVLGNSKSTPPASSEVVLDSK 246

Db 1624 -EMAEQVDQLNKLKAKAE-----HNR-----QTCNELNQTRTACDQLGRD-K 1664

Qy 247 RQVEKEE-----TNEIQ-----VNEEPQDRRLPOEPGRQVVEDRPVGGRGFGGAGELGQ 297

Db 1665 AEKEKNEYVQLNDLRAGVDHITNEKAAQEKI-----AKQLQH 1702

Qy 298 T-PQVQAALSVSQENPEMEGPERDQVLPDG-----QBEQEBAAGEGRNQKLRGEDDYNM 352

Db 1703 TLNEVQSKLDENRTNLTDFDASKKLSIENSDLLRQLEEAESQVLSKIKISLTQLED 1762

Qy 353 DENEAESETDKQAALAGNDRNI--DVFN-----VEDQKRDITNLLDQREKN 397

Db 1763 TKRLADEESRERATLLGKFRNLEHDLNLRQVEEAEGKADLQRLQSKAN 1813

RESULT 15

B32491

myosin heavy chain 2, muscle - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: B32491

R:George, E.L.; Ober, M.B.; Emerson Jr., C.P.

Mol. Cell. Biol. 9, 2957-2974, 1989

A:Title: Functional domains of the Drosophila melanogaster muscle myosin heavy-chain gene

A:Reference number: A32491; MUID:89384556; PMID:2506434

A:Accession: B32491

A:Status: preliminary

A:Molecule type: DNA; mRNA

A:Residues: 1-2411 <GEO>

A:Cross-references: UNIPROT:P05661; GB:M61229; GB:M27194

A:Note: the authors translated the codon TGC for residue 329 as Ser

C:Genetics:

A:Gene: FlyBase:Mhc

A:Cross-references: FlyBase:FBgn0002741

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: ATP; nucleotide binding; P-loop

F:137-1032/Domain: myosin motor domain homology #status atypical <MMO>

F:227-234/Region: nucleotide-binding motif A (P-loop)

Query Match 8.4%; Score 170; DB 2; Length 2411;

Best Local Similarity 20.9%; Pred. No. 0.42;

Matches 86; Conservative 77; Mismatches 148; Indels 100; Gaps 14;

Qy 41 LQTRIMELEGRVRRRAAARGAVELKNEFGQ-----ELEKQREOLDKIQSSHNQ 90

Db 1449 LEQTLDELEDSLEREKVKRGDVEKSKRVGDLKLTQEAVALDLERNKKELEQTQKDK 1508

Qy 91 LESVNLKYQDEKAVLVNNTTGERLIRVLQDLKTLQRYNGRLQDVLQFQKN----- 143

Db 1509 LSSITAKLEDEQVVVLKH---QRQIKELQARIBELEVEAEQARAKAQKQADLARE 1564

Qy 144 -----QTNLERKFSYDLSCINQMKEVKQCEBIEEVTYKKGNEAVAS 186

Db 1565 LEELGERLEEAGGATSAQIELNKKREAELSCLRDLDEEANTQHESTLANLRKKHNDAVA- 1623

Qy 187 RDLSENNDQROQLALSEPQPRLOAAGLPHTVEVPGKGNVLGNSKSTPPASSEVVLDSK 246

Db 1624 -EMAEQVDQLNKLKAKAE-----HNR-----QTCNELNQTRTACDQLGRD-K 1664

Qy 247 RQVEKEE-----TNEIQ-----VNEEPQDRRLPOEPGRQVVEDRPVGGRGFGGAGELGQ 297

Db 1665 AEKEKNEYVQLNDLRAGVDHITNEKAAQEKI-----AKQLQH 1702

Qy 298 T-PQVQAALSVSQENPEMEGPERDQVLPDG-----QBEQEBAAGEGRNQKLRGEDDYNM 352

Db 1703 TLNEVQSKLDENRTNLTDFDASKKLSIENSDLLRQLEEAESQVLSKIKISLTQLED 1762

Qy 353 DENEAESETDKQAALAGNDRNI--DVFN-----VEDQKRDITNLLDQREKN 397

Db 1763 TKRLADEESRERATLLGKFRNLEHDLNLRQVEEAEGKADLQRLQSKAN 1813

Search completed: June 7, 2005, 14:11:01

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